



CC rheumatoid arthritis  
XX Sequence 76 AA;

Query Match 100.0%; Score 394; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred. No. 1.1e-39;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKELDPIQKLFVDKIREYKSKRQTSGGPVDASSEYQOELERELFKLKOMFGNADMTPT 60  
DB 1 NKELDPIQKLFVDKIREYKSKRQTSGGPVDASSEYQOELERELFKLKOMFGNADMTPT 60

QY 61 FKFEDEPKFEVLEKPOA 76  
DB 61 FKFEDEPKFEVLEKPOA 76

RESULT 2  
AAG75820  
ID AAG75820 standard; protein; 84 AA.

XX AAG75820;

DT 03-SEP-2001 (first entry)

DE Human colon cancer antigen protein SEQ ID NO:6584.

KM Human colon cancer; colon cancer antigen; diagnosis; detection;

KW colorectal carcinoma; chromosome 10.

OS Homo sapiens.

PN WO200122920-A2.

PD 05-APR-2001.

PF 28-SEP-2000; 2000WO-US026524.

PR 29-SEP-1999; 99US-0157137P.

PR 03-NOV-1999; 99US-0163280P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Barash SC, Birse CE, Rosen CA;

DR WPI; 2001-235357/24.

DR N-PSDB; AAH35225.

PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
useful for preventing, diagnosing and/or treating colorectal cancers.

PS Claim 11; Page 8060-8062; 9803pp; English.

XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
cancer-associated nucleic acid molecules (N) and proteins (P), where the  
proteins are collectively known as colon cancer antigens. The colon  
cancer antigens have cytostatic activity and can be used in gene therapy  
and vaccine production. N and P may be used in the prevention, diagnosis  
and treatment of diseases associated with inappropriate P expression. For  
example, N and P may be used to treat disorders associated with decreased  
expression by rectifying mutations or deletions in a patient's genome  
that affect the activity of P by expressing inactive proteins or to  
supplement the patient's own production of P. Additionally, N may be used  
to produce the colon cancer-associated Ps, by inserting the nucleic acids  
into a host cell and culturing the cell to express the proteins. N and P  
can be used in the prevention, diagnosis and treatment of colorectal  
carcinomas and cancers. AAH37196 to AAH37204 and AAG77789 represent  
sequences used in the exemplification of the present invention. N.B.  
Pages 666 to 682 and page 7053 of the sequence listing were missing at  
time of publication, meaning no sequences are present for SEQ ID NO:1027  
to 1052, 7921 and 7922

XX Sequence 84 AA;

Query Match 99.5%; Score 392; DB 4; Length 84;  
Best Local Similarity 98.7%; Pred. No. 2.1e-39;  
Matches 75; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKELDPIQKLFVDKIREYKSKRQTSGGPVDASSEYQOELERELFKLKOMFGNADMTPT 60  
DB 9 NKELDPIQKLFVDKIREYKSKRQTSGGPVDASSEYQOELERELFKLKOMFGNADMTPT 68

QY 61 FKFEDEPKFEVLEKPOA 76  
DB 69 FKFEDEPKFEVLEKPOA 84

RESULT 3  
AAV48588  
ID AAV48588 standard; protein; 108 AA.

XX AAV48588;

DT 08-DEC-1999 (first entry)

DE Human breast tumour-associated protein 49.

KM Expressed sequence tag; EST; human; breast; cancer; gene therapy;  
treatment; tumour; cytostatic; medicament.

OS Homo sapiens.

PN DE19813839-A1.

PD 23-SEP-1999.

PF 20-MAR-1998; 98DE-01013839.

PR 20-MAR-1998; 98DE-01013839.

PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

PI Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;

DR WPI; 1999-528981/45.

DR N-PSDB; AA233657.

PT Human nucleic acid sequences and protein products from tumor breast  
tissue, useful for breast cancer therapy.

PS Claim 22; 164; 188pp; German.

XX This invention describes novel human nucleic acid sequences from tumor  
breast tissue which have cytostatic activity. The nucleic acid sequences  
can be used to produce and isolate full-length gene sequences. They can  
be used to express proteins, which can be used as tools to find an  
activity against breast cancer. The sequences can be used in sense or  
antisense form. They are especially useful for medicaments for gene  
therapy to treat breast cancer. AAV48540-Y48617 represent protein  
fragments encoded by the expressed sequence tags described in the method  
of the invention

XX Sequence 108 AA;

Query Match 99.5%; Score 392; DB 2; Length 108;  
Best Local Similarity 98.7%; Pred. No. 2.9e-39;  
Matches 75; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKELDPIQKLFVDKIREYKSKRQTSGGPVDASSEYQOELERELFKLKOMFGNADMTPT 60  
DB 33 NKELDPIQKLFVDKIREYKSKRQTSGGPVDASSEYQOELERELFKLKOMFGNADMTPT 92

QY 61 FKFEDEPKFEVLEKPOA 76  
DB 93 FKFEDEPKFEVLEKPOA 108

RESULT 4  
AAG04005  
ID AAG04005 standard; protein; 108 AA.  
XX  
AC AAG04005;  
XX  
DT 06-OCT-2000 (first entry)  
XX  
DE Human secreted protein, SEQ ID NO: 8086.  
XX  
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping.  
XX  
OS Homo sapiens.  
XX  
PN EP1033401-A2.  
XX  
PD 06-SEP-2000.  
XX  
PE 21-FEB-2000; 2000EP-00200610.  
XX  
PR 26-FEB-1999; 99US-0122487P.  
XX  
PA (GENT ) GENSET.  
XX  
PI Dunas Milne Edwards J, Duclert A, Giordano J;  
XX  
DR WPI; 2000-500381/45.  
DR N-PSDB; AAC04011.  
XX  
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.  
XX  
PS Claim 13; SEQ ID NO 8086; 71pp + Sequence listing; English.  
XX  
CC The present sequence is a polypeptide encoded by one of a large number of  
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different  
CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
CC region (UTR) of the mRNA because they are often obtained from oligo-dT  
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
CC clones derived from the 5' ends of mRNAs and even in those cases where  
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
CC are also used in diagnostic, forensic, gene therapy and chromosome  
CC mapping procedures. They are used to obtain upstream regulatory sequences  
CC and to design expression and secretion vectors  
XX  
SQ Sequence 108 AA:  
Query Match 99.5%; Score 392; DB 3; Length 108;  
Best Local Similarity 98.7%; Pred. No. 2.9e-39;  
Matches 75; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NKEIDPIQKLFVDKIREYKSRQTSGGPVDAASSEYQGLERELFKLKMFGNADMTPT 60  
DB 33 NKEIDPIQKLFVDKIREYKSRQTSGGPVDAASSEYQGLERELFKLKMFGNADMTPT 92  
QY 61 FKFDPKFEVLEKPOA 76  
DB 93 FKFDPKFEVLEKPOA 108  
XX  
RESULT 5  
ADE63626  
ID ADE63626 standard; protein; 108 AA.  
XX  
AC ADE63626;  
XX  
DT 29-JAN-2004 (first entry)

XX  
DE Human Protein P18859, SEQ ID NO 9570.  
XX  
KW Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
OS Homo sapiens.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PE 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GENO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'Urso D, Befort K, Costigan M;  
XX  
DR WPI; 2003-268312/26.  
DR GENBANK; P18859.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1; Page; 1017pp; English.  
XX  
CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 108 AA:  
Query Match 99.5%; Score 392; DB 7; Length 108;  
Best Local Similarity 98.7%; Pred. No. 2.9e-39;  
Matches 75; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 NKEIDPIQKLFVDKIREYKSRQTSGGPVDAASSEYQGLERELFKLKMFGNADMTPT 60  
DB 33 NKEIDPIQKLFVDKIREYKSRQTSGGPVDAASSEYQGLERELFKLKMFGNADMTPT 92  
QY 61 FKFDPKFEVLEKPOA 76  
DB 93 FKFDPKFEVLEKPOA 108

## RESULT 6

ADE63638  
ID ADE63638 standard; protein, 108 AA.

ADE63638;

29-JAN-2004 (first entry)

Human Protein P18859, SEQ ID NO 9582.

Human; pain; neuronal tissue; gene therapy;  
spinal segmental nerve injury; chronic constriction injury; CCI;  
spared nerve injury; SNI; Chung.

Homo sapiens.

MO2003016475-A2.

27-FEB-2003.

14-AUG-2002; 2002MO-US025765.

14-AUG-2001; 2001US-0312147P.

01-NOV-2001; 2001US-0346382P.

26-NOV-2001; 2001US-0333347P.

(GENO) GEN HOSPITAL CORP.

(FARB) BAYER AG.

Wolff C, D'urso D, Befort K, Costigan M;

WPI; 2003-268312/26.

GENBANK; P18859.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 108 AA;

Query Match 99.5%; Score 392; DB 7; Length 108;  
Best Local Similarity 98.7%; Pred. No. 2.9e-39;

Matches 75; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NKEIDPIQKLFVDRIRYKSKRQTSQGPVDSSEYQOELRELFKIKOMGNADMTFFPT 60

Db 33 NKEIDPIQKLFVDRIRYKSKRQTSQGPVDSSEYQOELRELFKIKOMGNADMTFFPT 92

Qy 61 FKFEDEPKFEVLEKRPQA 76

Db 93 FKFEDEPKFEVLEKRPQA 108

## RESULT 7

ADE63634  
ID ADE63634 standard; protein, 108 AA.

ADE63634;

29-JAN-2004 (first entry)

Human Protein P18859, SEQ ID NO 9578.

Human; pain; neuronal tissue; gene therapy;  
spinal segmental nerve injury; chronic constriction injury; CCI;  
spared nerve injury; SNI; Chung.

Homo sapiens.

MO2003016475-A2.

14-AUG-2002; 2002MO-US025765.

27-FEB-2003.

14-AUG-2001; 2001US-0312147P.

01-NOV-2001; 2001US-0346382P.

26-NOV-2001; 2001US-0333347P.

(GENO) GEN HOSPITAL CORP.

(FARB) BAYER AG.

Wolff C, D'urso D, Befort K, Costigan M;

WPI; 2003-268312/26.

GENBANK; P18859.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of



XX This invention relates to novel mitochondrial targets that can be used  
CC for therapeutic intervention in treating a disease associated with  
CC altered mitochondrial function. Specifically, it refers to a method for  
CC identifying proteins of the human heart mitochondrial proteome that are  
CC useful for drug screening assays, as well as therapeutic targets. The  
CC present invention describes a method for identifying such proteins that  
CC can be used in the treatment of various diseases associated with altered  
CC mitochondrial function including diabetes mellitus, Huntington's disease,  
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial  
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy  
CC tagged red fibre syndrome (MERRF) or cancer. Accordingly, these  
CC compositions have neuroprotective, neurotropic, antidiabetic,  
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and  
CC cytoskeletal activities. This polypeptide sequence is a human heart  
CC mitochondrial protein of the invention.

XX  
SQ Sequence 108 AA;

Query Match 99.5%; Score 392; DB 7; Length 108;  
Best Local Similarity 98.7%; Pred. No. 2.9e-39;  
Matches 75; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKEIDPIQKLFVDKIREYKSKRQTSGGPVDASSEYQOELERELFKLKQMGFNADMTPT 60  
DB 33 NKEIDPIQKLFVDKIREYKSKRQTSGGPVDASSEYQOELERELFKLKQMGFNADMTPT 92  
QY 61 FKPEDPKFEVLEKPOA 76  
DB 93 FKPEDPKFEVLEKPOA 108

RESULT 10  
AAAG01886  
ID AAG01886 standard; protein; 106 AA.  
AC AAG01886;  
DT 06-OCT-2000 (first entry)  
XX Human secreted protein, SEQ ID NO: 5967.  
DE Human secreted protein, SEQ ID NO: 5967.  
XX Human, 5' EST, expressed sequence tag; secreted protein; cDNA isolation;  
KW gene therapy; chromosome mapping.  
XX Homo sapiens.  
OS  
XX EPI033401-A2.  
FN 06-SEP-2000.  
XX 21-FEB-2000; 2000EP-00200610.  
PF 26-FEB-1999; 99US-0122487P.  
PR (GEST ) GENSET.  
XX  
PI Dunas Milne Edwards J, Duclert A, Giordano J;  
XX WPI; 2000-500381/45.  
DR N-PSDB; AAC01892.  
XX  
PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.  
XX  
XX Claim 13; SEQ ID NO 5967; 71pp + Sequence Listing; English.

CC The present sequence is a polypeptide encoded by one of a large number of  
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
CC prepared from total human RNAs or polyA<sup>+</sup> RNAs derived from 30 different  
CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
CC region (UTR) of the mRNA because they are often obtained from oligo-dT

CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
CC sequences derived from the 5' ends of mRNAs and even in those cases where  
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs  
CC are also used in diagnostic, forensic, gene therapy and chromosome  
CC mapping procedures. They are used to obtain upstream regulatory sequences  
CC and to design expression and secretion vectors

XX  
SQ Sequence 106 AA;

Query Match 97.2%; Score 383; DB 3; Length 106;  
Best Local Similarity 98.6%; Pred. No. 3.5e-38;  
Matches 73; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKEIDPIQKLFVDKIREYKSKRQTSGGPVDASSEYQOELERELFKLKQMGFNADMTPT 60  
DB 33 NKEIDPIQKLFVDKIREYKSKRQTSGGPVDASSEYQOELERELFKLKQMGFNADMTPT 92  
QY 61 FKPEDPKFEVLEKPOA 74  
DB 93 FKPEDPKFEVLEKPOA 106

RESULT 11  
AAAG7500  
ID AAG7500 standard; protein; 114 AA.  
AC AAG7500;  
DT 22-FEB-1999 (first entry)  
XX Human mitochondrial F6 subunit (HMF6) polypeptide.  
DE Human mitochondrial F6 subunit; HMF6; recombinant; cancer; treatment;  
KW ATP synthase coupling factor; myopathy; neurodegenerative disease.  
XX  
OS Homo sapiens.  
XX  
XX US5849527-A.  
FN 15-DEC-1998.  
XX 31-MAR-1997; 97US-00828239.  
PF 31-MAR-1997; 97US-00828239.  
PR 31-MAR-1997; 97US-00828239.  
XX (INCY-) INCYTE PHARM INC.  
XX  
XX Hillman JL, Shah P;  
XX WPI; 1999-069728/06.  
DR N-PSDB; AAV80300.  
XX  
PT DNA encoding human mitochondrial F6 subunit polypeptide - useful for  
PT producing recombinant polypeptide or as probe.  
XX  
XX Claim 1; Fig 1A-B; 26pp; English.

CC This represents a human mitochondrial F6 subunit (HMF6) polypeptide. Host  
CC cells comprising a vector containing the HMF6 nucleic acid can be used  
CC for the recombinant production of the protein. The HMF6 polypeptide is a  
CC novel ATP synthase coupling factor and may be used in the treatment of  
CC cancer, myopathies and neurodegenerative diseases. The nucleic acid can  
CC be used as a probe to detect HMF6 genes

XX  
SQ Sequence 114 AA;

Query Match 82.5%; Score 325; DB 2; Length 114;  
Best Local Similarity 98.4%; Pred. No. 3.9e-31;  
Matches 62; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 KIREYKSKRQTSGGPVDASSEYQOELERELFKLKQMGFNADMTPTFKPEDPKFEVLEK 73

Db 52 KIREYKSRKQTSGGVVDASSEYQOELERELFKLKMFGNADNPTPTFKFEDPKFEVLEK 111  
 QY 74 POA 76  
 112 POA 114

RESULT 12  
 AAY82605  
 ID AAY82605 standard; protein; 114 AA.

AC AAY82605;  
 DT 02-AUG-2000 (first entry)

DE Human mitochondrial F6 subunit protein sequence SEQ ID NO:1.

XX Human; mitochondrial F6 subunit; HMF6; cytosolic; noctropic;  
 KM neuroprotective; antiparkinsonian; anticonvulsant; gene therapy; cancer;  
 KM myopathy; external ophthalmoplegia; Kearns-Sayre syndrome;  
 KM lactic acidosis; neurodegenerative disorder; Alzheimer's disease;  
 KM Huntington's disease; Parkinson's disease; epilepsy.

OS Homo sapiens.

PN US6048718-A.

PD 11-APR-2000.

PF 04-DEC-1998; 98US-00205679.

PR 31-MAR-1997; 97US-00828239.

PA (INCY-) INCYTE PHARM INC.

PI Shah P, Hillman JL;

DR WPI: 2000-302782/26.

DR N-P8DB; AAA13916.

XX Purified human mitochondrial F6 subunit polypeptide is useful for  
 PT treating cancer, myopathy e.g. ophthalmoplegia, Kearns-Sayre syndrome and  
 PT neurodegenerative disorders e.g. Alzheimer's disease and epilepsy.

XX Claim 1; Fig 1; 27pp; English.

XX The present sequence represents the human mitochondrial F6 subunit (HMF6)  
 CC protein. HMF6 has cytosolic, noctropic, neuroprotective,  
 CC antiparkinsonian and anticonvulsant activities, and can be used in gene  
 CC therapy. HMF6 is useful in a composition in conjunction with a suitable  
 CC carrier for treating cancer, myopathies such as external ophthalmoplegia,  
 CC Kearns-Sayre syndrome, lactic acidosis and neurodegenerative disorders  
 CC such as Alzheimer's disease, Huntington's disease, Parkinson's disease  
 CC and epilepsy

XX Sequence 114 AA;

Query Match 82.5%; Score 325; DB 3; Length 114;  
 Best Local Similarity 98.4%; Pred. No. 3.9e-31;  
 Matches 62; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 KIREYKSRKQTSGGVVDASSEYQOELERELFKLKMFGNADNPTPTFKFEDPKFEVLEK 73  
 DB 52 KIREYKSRKQTSGGVVDASSEYQOELERELFKLKMFGNADNPTPTFKFEDPKFEVLEK 111

QY 74 POA 76  
 112 POA 114

RESULT 13  
 AAB80964

ID AAB80964 standard; protein; 76 AA.

XX AAB80964;

AC AAB80964;  
 DT 08-JUN-2001 (first entry)

DE Rat Coupling factor 6 CF6.

XX Rat; coupling factor 6; CF6; antiinflammatory; antidiabetic; antiulcer;  
 KM cardiact; hypotensive; antianginal; antiaesthetic; antirheumatic;  
 KM antiarthritic; proton-translocating ATPase; prostaglandin;  
 KM cytoplasmic PLA<sub>2</sub>; cardiovascular disorder; diabetes;  
 KM inflammatory disorder; rheumatoid arthritis; cerebrovascular disorder.

OS Rattus sp.

PN WO200121205-A1.

PD 29-MAR-2001.

PF 03-AUG-2000; 2000WO-JP005210.

PR 17-SEP-1999; 99JP-00264687.

PA (SUNR ) SUNTORY LTD.

PI Osanai T, Magoita K;

DR WPI: 2001-266047/27.

PT Coupling factor 6 useful in diagnosis of diseases relating to excess or  
 PT lack of prostaglandin and cytoplasmic PLA<sub>2</sub> activity in blood, and in  
 PT screening drugs for treating e.g. cardiovascular infarction.

XX Claim 15; Page 56-7; 70pp; Japanese.

XX The present sequence is rat coupling factor 6 (CF6) protein. CF6 is a  
 CC subunit of a proton-translocating ATPase found in mitochondria. CF6 can  
 CC be used in diagnosis of diseases relating to excess or lack of  
 CC prostaglandin and cytoplasmic PLA<sub>2</sub> activity, and in screening inhibitors  
 CC and potentiators as drugs to treat e.g. cardiovascular infarction,  
 CC hypertension, arteriosclerosis, angina pectoris, cardiac insufficiency,  
 CC cerebrovascular disorders, hyperlipemia, diabetes, bronchiolitis, gastric  
 CC ulcer, pregnant eclampsia, haemolytic uremia syndrome, thrombopenic  
 CC purpura, inflammatory diseases like cerebral infarction, acute  
 CC pancreatitis, asthma, ARDS (adult respiratory distress syndrome), and  
 CC rheumatoid arthritis

XX Sequence 76 AA;

Query Match 80.5%; Score 317; DB 4; Length 76;  
 Best Local Similarity 75.0%; Pred. No. 2.2e-30;  
 Matches 57; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 NKEIDPIQKLFVDRKIREYKSRKQTSGGVVDASSEYQOELERELFKLKMFGNADNPTPT 60  
 DB 1 NKEIDPIQKLFVDRKIREYKSRKQTSGGVVDGTPETQOEVDRKELFKLKMFGNADNPTPT 60

QY 61 FKFEDEPKFEVLEKPOA 76  
 DB 61 FKFEDEPKFEVLEKPOA 76

RESULT 14  
 ADE63636  
 ID ADE63636 standard; protein; 108 AA.

AC ADE63636;

DT 29-JAN-2004 (first entry)

DE Rat Protein P21571, SEQ ID NO 9580.

	Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KM	Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX	
OS	Rattus norvegicus.
PX	
PN	MO2003016475-A2.
PD	
XX	27-FEB-2003.
PF	
PP	14-AUG-2002; 2002WO-US025765.
PR	
PR	14-AUG-2001; 2001US-0312147P.
PR	01-NOV-2001; 2001US-0346382P.
PR	26-NOV-2001; 2001US-0333347P.
PA	(GENO ) GEN HOSPITAL CORP.
PA	(FARB ) BAYER AG.
XX	
PI	Woolf C, D'urso D, Befort K, Costigan M,
DR	WPI; 2003-268312/26.
XX	
DR	GENBANK; P21571.
PT	
PT	New composition comprising two or more isolated polypeptides, useful for
XX	preparing a medicament for treating pain in an animal.
PS	
XX	Claim 1; Page; 1017pp; English.
CC	The invention discloses a composition comprising two or more isolated rat
CC	or human polynucleotides or a polynucleotide which represents a fragment,
CC	derivative or allelic variation of the nucleic acid sequence. Also
CC	claimed are a vector comprising the novel polynucleotide, a host cell
CC	comprising the vector, a method for identifying a nucleotide sequence
CC	which is differentially regulated in an animal subjected to pain and a
CC	kit to perform the method, an array, a method for identifying an agent
CC	that increases or decreases the expression of the polynucleotide sequence
CC	that is differentially expressed in neuronal tissue of a first animal
CC	subjected to pain, a method for identifying a compound which regulates
CC	the expression of a polynucleotide sequence which is differentially
CC	expressed in an animal subjected to pain, a method for identifying a
CC	compound that regulates the activity of one or more of the
CC	polynucleotides, a method for producing a pharmaceutical composition, a
CC	method for identifying a compound or small molecule that regulates the
CC	activity in an animal of one or more of the polypeptides given in the
CC	specification, a method for identifying a compound useful in treating
CC	pain and a pharmaceutical composition comprising the one or more
CC	polypeptides or their antibodies. The polynucleotide or the compound that
CC	modulates its activity is useful for preparing a medicament for treating
CC	pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC	injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC	therapy). The sequence presented is a rat protein (shown in Table 2 of
CC	the specification) which is differentially expressed during pain. Note:
CC	The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic form directly from WIPO at
CC	ftp.wipo.int/pub/published_pat_sequences.
XX	
SQ	Sequence 108 AA:
Query Match	80.5%; Score 317; DB 7; Length 108;
Best Local Similarity	75.0%; Pred. No. 3.3e-30;
Matches	57; Conservative 10; Mismatches 9; Indels 0; Gaps 0
Dd	
1	NKELDLPYOKL FVKIRIPEYSKRGOTSGGPVDASSEVOGEERELFTLKMGFGNADNNPPT 60
	:           :           :           :
33	NKELDLPYOKLFLLDIRIRYKANRLASGAPVDTPGEIVQGEVRELFYTKMYGTGGENDKFPT 92
Oy	
61	FKFEDPKFEVLDEKQA 76
	:           :           :
Db	
93	FNFDPKFEVLDEKQS 108

ID	ADBE63632 standard; protein; 108 AA.
XX	
AC	ADBE63632;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Rat Protein P21571, SRQ ID NO 9576.
XX	
KW	Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW	chronic constriction injury; CCI, spared nerve injury; SNI; Chung.
XX	
OS	Rattus norvegicus.
XX	
PN	WO2003016475-A2.
XX	
PD	27-FEB-2003.
XX	
PF	14-AUG-2002; 2002WO-US025765.
XX	
PR	14-AUG-2001; 2001US-0312147P.
PR	01-NOV-2001; 2001US-0346382P.
PR	26-NOV-2001; 2001US-0333347P.
XX	
PA	(GEHO ) GEN HOSPITAL CORP.
PA	(FARB ) BAYER AG.
XX	
PI	Woolf C, D'Urso D, Befort K, Costigan M;
XX	
PI	WPI; 2003-268312/26.
DR	GENBANK; P21571.
XX	
PT	New composition comprising two or more isolated polypeptides, useful for
PT	preparing a medicament for treating pain in an animal.
XX	
PS	Claim 1; Page; 1017Pp; English.
XX	
XX	The invention discloses a composition comprising two or more isolated rat
CC	or human polynucleotides or a polynucleotide which represents a fragment,
CC	derivative or allelic variation of the nucleic acid sequence. Also
CC	claimed are a vector comprising the novel polynucleotide, a host cell
CC	comprising the vector, a method for identifying a nucleotide sequence
CC	which is differentially regulated in an animal subjected to pain and a
CC	kit to perform the method, an array, a method for identifying an agent
CC	that increases or decreases the expression of the polynucleotide sequence
CC	that is differentially expressed in neuronal tissue of a first animal
CC	subjected to pain, a method for identifying a compound which regulates
CC	the expression of a polynucleotide sequence which is differentially
CC	expressed in an animal subjected to pain, a method for identifying a
CC	compound that regulates the activity of one or more of the
CC	polynucleotides, a method for producing a pharmaceutical composition, a
CC	method for identifying a compound or small molecule that regulates the
CC	activity in an animal of one or more of the polypeptides given in the
CC	specification, a method for identifying a compound useful in treating
CC	pain and a pharmaceutical composition comprising the one or more
CC	polypeptides or their antibodies. The polynucleotide or the compound that
CC	modulates its activity is useful for preparing a medicament for treating
CC	pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
CC	therapy). The sequence presented is a rat protein (shown in Table 2 of
CC	the specification) which is differentially expressed during pain. Note:
CC	The sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic form directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences.
XX	
XX	Sequence 108 AA;
XX	
Query Match	80.5%; Score 317; DB 7; Length 108;
Best Local Similarity	75.0%; Pred. No. 3,3e-30;
Matches	57; Conservative 10; Mismatches 9; Indels 0; Gaps 0
QY	1 NKEALPDIKLFVDFKTRKYSKQTSGGPVDASSEYQOELERELFTLKQKMGFADNNTPT 60
DB	33 NKEALPVDQGLFDFDKTRKYSKRLASGGFVDTSPEYQOEVDRRLFTLKQKMGFADNNTPT 92



Oy 61 FKFEPPKFEVLEKPOA 76  
| | | | | : | | | | |  
Db 93 FNFEDPKFEVLEKPOA 108

Search completed: April 4, 2005, 19:19:22  
Job time : 127.5 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 4, 2005, 18:59:30 ; Search time 118.5 Seconds  
(without alignments)  
328.422 Million cell updates/sec

Title: US-09-831-951A-2  
Perfect score: 402  
Sequence: 1 NKEIDPYQKFLDKIRRYKA.....KPTFNFEDPKFEVLDRKQS 76

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	402	100.0	108	1	ATPR_RAT
2	358	89.1	108	1	ATPR_MOUSE
3	333	82.8	108	1	ATPR_BOVIN
4	331	82.3	108	1	Q8SPH6
5	329	81.8	76	1	ATPR_PIG
6	315	78.4	108	1	ATPR_HUMAN
7	306	76.1	108	2	Q6NZ59
8	241	60.0	107	2	Q6PG55
9	238	59.2	107	2	Q6FR11
10	198	49.3	112	2	Q6NYF7
11	162	40.3	117	2	Q7Q7P4
12	156.5	38.9	106	1	ATPR_DROME
13	132.5	33.0	147	2	Q9VZ72
14	106	26.4	54	2	Q8I2D0
15	80.5	20.0	285	2	Q6R840
16	77.5	19.3	578	2	Q05924
17	76.5	19.0	219	2	Q750B1
18	75.5	18.8	1654	2	Q8FM04
19	75	18.7	1454	2	Q7ZMK4
20	74	18.4	143	2	Q8YVU3
21	74	18.4	1196	2	Q8PM00
22	72.5	18.0	858	2	Q17647
23	72.5	18.0	860	2	Q95NM4
24	71.5	17.8	1405	2	Q22691
25	71	17.7	382	2	Q93516
26	70.5	17.5	262	2	Q82HA2
27	70.5	17.5	1934	2	Q75UR1
28	70	17.4	570	2	Q7UH95
29	69	17.4	1103	2	Q64X88
30	68.5	17.0	1242	2	Q6CNK0
31	68	16.9	210	2	Q6C3F2

32	68	16.9	385	2	Q8K687	Q8K687 streptococ
33	68	16.9	1919	2	Q7RRU1	Q7RRU1 plasmodium
34	68	16.9	2719	2	Q7RP10	Q7RP10 plasmodium
35	67	16.7	322	2	Q6APB7	Q6APB7 desulfotale
36	67	16.7	797	2	Q67651	Q67651 aquilex aeo
37	67	16.7	914	2	Q8S5Q7	Q8S5Q7 oryza sativ
38	67	16.7	976	2	Q6FKX5	Q6FKX5 candida gla
39	67	16.7	996	2	Q24303	Q24303 pisum sativ
40	67	16.7	1140	2	Q7PDD7	Q7PDD7 plasmodium
41	66.5	16.5	425	2	Q6MM03	Q6MM03 bdellovibri
42	66.5	16.5	458	2	Q8IUS8	Q8IUS8 homo sapien
43	66.5	16.5	458	2	Q6UWV6	Q6UWV6 homo sapien
44	66.5	16.5	531	2	Q6ZTS5	Q6ZTS5 homo sapien
45	66	16.4	101	2	Q8EN19	Q8EN19 oceanobacil

## ALIGNMENTS

```

RESULT 1
ATPR_RAT      STANDARD;      PRT;      108 AA.
ID   ATPR_RAT
AC   P21571;
DT   01-MAY-1991 (Rel. 18, Created)
DR   01-MAY-1991 (Rel. 18, Last sequence update)
DS   05-JUL-2004 (Rel. 44, Last annotation update)
DE   ATP synthase coupling factor 6, mitochondrial precursor (EC 3.6.3.14)
DE   (FE).
GN   Name=Atp5f1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
XP   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Liver;
RX   MEDLINE=91024964; PubMed=2145831;
RA   Higuti T., Osaka F., Yoshihara Y., Tsurumi C., Kawamura Y., Tani I.,
RA   Toda H., Kakuno T., Sakiyama F., Tanaka K., Ichihara A.;
RT   "cDNA cloning and sequencing for the import precursor of coupling
RT   factor 6 in H(+)-ATP synthase from rat liver mitochondria.";
RL   Biochem. Biophys. Res. Commun. 171:1079-1086(1990).
[2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Anterior pituitary;
RX   MEDLINE=92339904; PubMed=1386054; DOI=10.1016/0378-1119(92)90528-W;
RA   Tracer H.L., Itoh Y.P., Birch N.P.;
RT   "Rat mitochondrial coupling factor 6: molecular cloning of a cDNA
RT   encoding the imported precursor.";
RL   Gene 116:291-292(1992).
[3]
RP   SEQUENCE OF 33-66.
RC   TISSUE=Liver;
RX   MEDLINE=93054567; PubMed=1429613;
RA   Higuti T., Yoshihara Y., Kuroiwa K., Kawamura Y., Toda H.,
RA   Sakiyama F.;
RT   "A simple, rapid method for purification of epsilon-subunit, coupling
RT   factor 6, subunit d, and subunit e from rat liver H(+)-ATP synthase
RT   and determination of the complete amino acid sequence of epsilon-
RT   subunit.";
RL   J. Biol. Chem. 267:22658-22661(1992).
[4]
RP   FUNCTION: This is one of the chains of the nonenzymatic component
RP   (CF0) subunit of the mitochondrial ATPase complex. F6 seems to
RP   be part of the stalk that links CF(0) to CF(1).
[5]
RP   - CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
RP   H(+) (Out).
[6]
RP   - SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic
RP   core - and CF(0) - the membrane proton channel. CF(0) seems to
RP   have nine subunits: a, b, c, d, e, f, g, F6 and 8 (or A6L).
[7]
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; M73030; AAA40954.1; -;  
 DR EMBL; X54510; CA38369.1; -;  
 DR PIR; J01167; J01167.  
 DR HSC-2DPAGE; P21571; RAT.  
 DR RCD; 621376; Alp5j.  
 DR InterPro: IPR00387; ATP synth\_F6.  
 DR Pfam; PF05511; ATP-synth\_F6; 1.  
 KW CF(0); Direct protein sequencing; Hydrogen ion transport;  
 KW Mitochondrion; Transit peptide.  
 FT TRANSIT 1 32  
 FT CHAIN 33 108 ATP synthase coupling factor 6.  
 SQ SEQUENCE 108 AA; 12494 MW; FFI177C9681B5F51 CRC64;

Query Match 100.0%; Score 402; DB 1; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 1,6e-34;  
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKEIDPVOKFLDKIRREYKAKRLASGGPVDTGPEYQOEVDRELFKLQMGKGMKXPT 60  
 DB 33 NKEIDPVOKFLDKIRREYKAKRLASGGPVDTGPEYQOEVDRELFKLQMGKGMKXPT 92

QY 61 FNFEDPKFEVLDKPOS 76  
 DB 93 FNFEDPKFEVLDKPOS 108

RESULT 2  
 ATPR MOUSE STANDARD; PRT; 108 AA.  
 ID ATPR MOUSE  
 AC P97450;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE ATP synthase coupling factor 6, mitochondrial precursor (EC 3.6.3.14)  
 DE (Fe).  
 GN Name=Atps5j;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA Roach D., Anderson E., Botcherby M., Jordan B., Carrier A.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6j;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nakai K., Otsu N., Saito K., Suzuki H., Yamana I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,  
 RA Baldarelli R., Hill D.P., Bull C., Hume D.A., Quackenbush J.,  
 RA Schiraldi L.M., Kanapin A., Mateuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bratt D., Brusic V., Chochua C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Giesli C., Godzik A., Gough J.,  
 RA Grimmond S., Guclincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Nimata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.V., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verrato R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilting L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kikukawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
 RA Shitaki T., Waki K., Kawai J., Aizawa K., Arkawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [3].  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Peltingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mallary S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,  
 RA Richey J., Krzywicki M.I., Skalska U., Smalins D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC - FUNCTION: This is one of the chains of the nonenzymatic component  
 CC (CF(0) subunit) of the mitochondrial ATPase complex. F6 seems to  
 CC be part of the stalk that links CF(0) to CF(1).  
 CC - CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +  
 CC H(+) (Out).  
 CC - SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic  
 CC core - and CF(0) - the membrane proton channel. CF(0) seems to  
 CC have nine subunits: a, b, c, d, e, f, g, F6 and 8 (or A6L).  
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DR EMBL; U77128; AAB19213.1; -;  
 DR EMBL; AK078484; BAC37301.1; -;  
 DR EMBL; BC010766; AAI10766.1; -;  
 DR SWISS-2DPAGE; P97450; MOUSE.  
 DR MGI; MGI:107777; Alp5j.  
 DR InterPro: IPR006187; ATP synth\_F6.  
 DR Pfam; PF05511; ATP-synth\_F6; 1.  
 KW CF(0); Hydrogen ion transport; Mitochondrion; Transit peptide.  
 FT TRANSIT 1 32  
 FT CHAIN 33 108 Mitochondrion (By similarity).  
 FT ATP synthase coupling factor 6.  
 SQ SEQUENCE 108 AA; 12496 MW; E2A2E63F723C8BF CRC64;

Query Match 89.1%; Score 356; DB 1; Length 108;  
 Best Local Similarity 85.5%; Pred. No. 6,8e-30;  
 Matches 65; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 NKEIDPVOKFLDKIRREYKAKRLASGGPVDTGPEYQOEVDRELFKLQMGKGMKXPT 60  
 DB 33 NKEIDPVOKFLDKIRREYKAKRLASGGPVDTGPEYQOEVDRELFKLQMGKGMKXPT 92

QY 61 FNFEDPKFEVLDKPOS 76  
 DB 93 FNFEDPKFEVLDKPOS 108

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DB          93  FKFPDDPKFEVIDKPKQS  108

RESULT  3
ATPR_BOVIN
ID  _ATPR_BOVIN  STANDARD;  PRT;  108 AA.
AC  P02721;
DT  21-JUL-1986 (Rel. 01, Created)
DT  01-JAN-1990 (Rel. 13, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  ATP synthase coupling factor 6, mitochondrial precursor (EC 3.6.3.14)
   (F6).
GN  Name=ATP5J;
OS  Bos taurus (Bovine).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovinae; Bos.
OX  NCBI_TaxID=9913;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=86163536; PubMed=2894843;
RA  Walker J.E., Gay N.J., Powell S.J., Kostina M., Dyer M.R.;
RT  "ATP synthase from bovine mitochondria: sequences of imported
RT  precursors of oligomycin sensitivity conferral protein, factor 6, and
RT  adenosine triphosphatase inhibitor protein."
RL  Biochemistry 26:8613-8619(1987).
RN  [2]
RP  SEQUENCE OF 33-108.
RX  MEDLINE=85038563; PubMed=6149548;
RA  Fang J.-K., Jacobs J.W., Kanner B.I., Rackner R., Bradshaw R.A.;
RT  "Amino acid sequence of bovine heart coupling factor 6."
RL  Proc. Natl. Acad. Sci. U.S.A. 81:6603-6607(1984).
RN  [3]
RP  SEQUENCE OF 33-37.
RX  TISSUE=Heart;
RA  MEDLINE=91242449; PubMed=1827992;
RT  Walker J.E., Lutter R., Dupuis A., Runswick M.J.;
RL  "Identification of the subunits of F1F0-ATPase from bovine heart
   mitochondria."
CC  Biochemistry 30:5369-5378(1991).
CC  -1- FUNCTION: This is one of the chains of the nonenzymatic component
   (CF(0) subunit) of the mitochondrial ATPase complex. F6 seems to
   be part of the stalk that links CF(0) to CF(1). Also involved in
   the restoration of oligomycin-sensitive ATPase activity to
   depleted F1-F0 complexes.
CC  -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate +
   H(+) (out).
CC  -1- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic
   core - and CF(0) - the membrane proton channel. CF(0) seems to
   have nine subunits: a, b, c, d, e, f, g, F6 and 8 (or delta).
CC  -----
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CC  -----
EMBL; M19317; AAA30511.1; -
DR  PIR; B27382; JLB06.
DR  InterPro; IPR008387; ATP_synth_F6.
DR  Pfam; PF05511; ATP_synth_F6; 1.
KW  CF(0); Direct protein sequencing; Hydrogen ion transport;
KW  mitochondrial; Transit peptide.
FT  TRANSIT 1
FT  CHAIN 33 108 Mitochondrion.
FT  CONFLICT 94 108 ATP synthase coupling factor 6.
FT  T 94 T -> F (in Ref. 2).
SQ  SEQUENCE 108 AA; 12532 MW; E5376A0518C3E1C8 CRC64;

Query Match      82.8%; Score 333; DB 1; Length 108;
Best Local Similarity 78.9%; Pred. No. 2.9e-27;
Matches 60; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

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Qy	1	NKELDPPVQKLELDKIREYKARLMSGGPGVDGPGEYQGSVDDELFLDKOMYGGSEWDRKPT	60
Db	33	NKELDPPVQKLELDKIREYKARLMSGGPGVDGPGEYQGSVDDELFLDKOMYGGSEWDRKPT	92
Qy	61	FNFDPKFEVLDKRPQS	76
Db	93	FTFEDPKFEVLEKRPQS	108
RESULT 4			
ID	Q8SPH6	PRELIMINARY;	PRT; 108 AA.
AC	Q8SPH6;		
DT	01-JUN-2002 (TREMBlrel. 21, Created)		
DT	01-JUN-2002 (TREMBlrel. 21, Last sequence update)		
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)		
DE	ATP synthase subunit F6.		
GN	Name=ATP5f;		
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;		
OC	Cercopithecinae; Macaca.		
OX	NCBI_TaxID=9541;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain parietal lobe;		
RA	Osada N., Kuwada J., Hirata M., Tanuma R., Hida M., Sugano S.,		
RA	Hirai M., Hashimoto K.;		
RT	"Search for genes positively selected during primate evolution by 5'-		
RT	end-sequence screening of cynomolgus monkey cDNAs.";		
RL	Genomics 79:657-662(2002).		
DR	EMBL; AB072025; BABB6814.1; "		
DR	GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.		
DR	GO; GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.		
DR	GO; GO:0046961; F:hydrogen-transporting ATPase activity; IEA.		
DR	GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.		
DR	InterPro; IPRO06387; ATP synth_F6; 1.		
DR	Pfam; PF05511; ATP-synt_F6; 1.		
DR	SEQUENCE 108 AA; 12587 MW; A33AC44891716C1E CRC64;		
Query Match 82.3%; Score 331; DB 2; Length 108;			
Best Local Similarity 79.7%; Pred. No. 4.7e-27;			
Matches 59; Conservative 10; Mismatches 5; Indels 0; Gaps 0;			
Qy	1	NKELDPPVQKLELDKIREYKARLMSGGPGVDGPGEYQGSVDDELFLDKOMYGGSEWDRKPT	60
Db	33	NKELDPPVQKLELDKIREYKARLMSGGPGVDGPGEYQGSVDDELFLDKOMYGGSEWDRKPT	92
Qy	61	FNFDPKFEVLDKRPQS	74
Db	93	FTFEDPKFEVLEKRPQS	106
RESULT 5			
ID	ATPR_PIG	STANDARD;	PRT; 76 AA.
AC	P13619;		
DT	01-JAN-1990 (Rel. 13, Created)		
DT	01-JAN-1990 (Rel. 13, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	ATP synthase coupling factor 6, mitochondrial (EC 3.6.3.14) (F6).		
GN	Name=ATP5f;		
OS	Sus scrofa (Pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
OX	NCBI_TaxID=9823;		
RN	[1]		
RP	SEQUENCE.		
RC	TISSUE=Intestine;		
RA	MEDLINE=88083634; PubMed=2961617; DOI=10.1016/0014-5793(87)80547-1;		
RA	Chen Z.-W., Malt V., Barros-Seoedling U., Joenavall H.;		
RT	"Isolation and structural characterization of porcine coupling factor		

RT 6 from intestinal tissues.";  
 CC PFBS Lett. 226:43-46(1987).  
 CC -1- FUNCTION: This is one of the chains of the nonenzymatic component  
 CC (CF(0) subunit) of the mitochondrial ATPase complex. F6 seems to  
 CC be part of the stalk that links CF(0) to CF(1).  
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate +  
 CC H(+) (out).  
 CC -1- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic  
 CC core - and CF(0) - the membrane proton channel. CF(0) seems to  
 CC have nine subunits: a, b, c, d, e, f, g, F6 and 8 (or A6L).  
 DR PIR: S00212; S00212.  
 DR Interpro: IPR008387; ATP\_synth\_F6.  
 DR Pfam: PF05511; ATP-synth\_F6; 1.  
 KM CF(0) ; Direct protein sequencing; Hydrogen ion transport;  
 KM Mitochondrion.  
 SQ SEQUENCE 76 AA; 8930 MW; 16F73EE42F87B874 CRC64;

Query Match 81.8%; Score 329; DB 1; Length 76;  
 Best Local Similarity 77.6%; Pred. No. 5.2e-27;  
 Matches 59; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 NKEIDPQKFLDKIRRYKAKRLASGGPVDTGPYQGEVDRFLKQMGKGMKEFPT 60  
 DB 1 NKEIDPQKFLVDKIRRYKRTKQTSQGPVDAQPEYQDLDRLFKLQMGKADMTFNP 60

QY 61 NFEDPKFEVLDKRPQS 76  
 DB 61 FTEDPKFEAVEKRPQS 76

RESULT 6  
 ATPR\_HUMAN STANDARD; PRT; 108 AA.  
 ID ATPR\_HUMAN  
 AC P18859;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE ATP synthase coupling factor 6, mitochondrial precursor (EC 3.6.3.14)  
 DE (F6).  
 GN Name=ATP5J; Synonyms=ATPM;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RX MEDLINE=9115516; PubMed=1830479;  
 RX MEDLINE=9115516; PubMed=1830479;  
 RA Hagiuti T., Tsurumi C., Kawamura Y., Tsujita H., Osaka F.,  
 RA Yoshizawa Y., Tani I., Tanaka K., Ichihara A.;  
 RT "Molecular cloning of cDNA for the import precursor of human coupling  
 RT factor 6 of H(+) -ATP synthase in mitochondria.";  
 RL Biochem. Biophys. Res. Commun. 178:793-799(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RP TISSUE=Kidney;  
 RX MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;  
 RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glaesli S.,  
 RA Anstoege W., Boecker M., Bloecker H., Baerachas S., Blum H.,  
 RA Lauber J., Duesterhoeft A., Beyer A., Koerner K., Strack N.,  
 RA Mewes H.-W., Ottensmeyer F., Obermaier B., Tampe J., Heubner D.,  
 RA Mambrot R., Korn B., Klein M., Poustka A.;  
 RT "Towards a catalog of human genes and proteins: sequencing and  
 RT analysis of 500 novel complete protein coding human cDNAs.";  
 RL Genome Res. 11:422-435(2001).  
 RP [4]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=20289799; PubMed=10690953; DOI=10.1038/35012518;  
 RA Hattori M., Fujiyama A., Taylor T.D., Matanabe H., Yada T.,  
 RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Seoda E.,  
 RA Onki H., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,  
 RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,  
 RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,  
 RA Rosenthal A., Kudoh T., Shibuya K., Kawasaki K., Asakawa S.,  
 RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,  
 RA Minoshima S., Shimizu N., Kordaslek G., Hornischer K., Brandt P.,  
 RA Scharte M., Schoen O., Dessato A., Reichelt U., Kauer G., Bloecker H.,  
 RA Ramser J., Beck A., Klages S., Hennig S., Risselmann L., Dagnand E.,  
 RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,  
 RA Leberich H., Reinhardt R., Vaspou M.-L.;  
 RT "The DNA sequence of human chromosome 21.";  
 RL Nature 405:311-319(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RP TISSUE=Eye;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uadiri T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millamy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Buttefield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Maria M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]  
 RP SEQUENCE OF 33-43.  
 RP TISSUE=Liver;  
 RX MEDLINE=93162045; PubMed=1286669;  
 RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,  
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargass R.,  
 RA Appel R.D., Hughes G.U.;  
 RT "Human liver protein map: a reference database established by  
 RT microsequencing and gel comparison.";  
 RL Electrophoresis 13:992-1001(1992).  
 CC -1- FUNCTION: This is one of the chains of the nonenzymatic component  
 CC (CF(0) subunit) of the mitochondrial ATPase complex. F6 seems to  
 CC be part of the stalk that links CF(0) to CF(1). Also involved in  
 CC the restoration of oligomycin-sensitive ATPase activity to  
 CC depleted F1-F0 complexes.  
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate +  
 CC H(+) (out).  
 CC -1- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic  
 CC core - and CF(0) - the membrane proton channel. CF(0) seems to  
 CC have nine subunits: a, b, c, d, e, f, g, F6 and 8 (or A6L).  
 CC -----  
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 CC -----  
 DR EMBL: M37104; AAA51807.1; -;  
 DR EMBL: M73031; AAA58630.1; -;  
 DR EMBL: AL110183; CAB53667.1; -;  
 DR EMBL: AP001694; -; NOT ANNOTATED\_CDS.  
 DR EMBL: BC001178; AAH01178.1; -;

DR PIR; JT0563; JT0563.  
DR SWISS-2DPAGE; P18859; HUMAN.  
DR Genem; HGNC:847; ATP5J.  
DR H-InVDB; HIX0016040; -.  
DR Reactome; P18859; -.  
DR MIM; 603152; -.  
DR GO; GO:0005743; C:mitochondrial inner membrane; TAS.  
DR GO; GO:0005739; C:mitochondrion; TAS.  
DR InterPro; IPR008387; ATP synth\_F6.  
DR Pfam; PF05511; ATP-synt\_F6; 1\_F6.  
DR CF(O); Direct protein sequencing; Hydrogen ion transport;  
KM Mitochondrion; Transit peptide;  
FT TRANSIT 1 32 Mitochondrion.  
FT CHAIN 33 108 ATP synthase coupling factor 6.  
FT CONFLICT 68 68 O -> H (in Ref. 2).  
SQ SEQUENCE 108 AA; 12587 MW; EDC1A4F01A10F17 CRC64;  
Query Match 78.4%; Score 315; DB 1; Length 108;  
Best Local Similarity 73.7%; Pred. No. 2,3e-25;  
Matches 56; Conservative 11; Mismatches 9; Indels 0; Gaps 0;  
QY 1 NKELDPIQKFLDIREYKAKRLASGGPVDTGPEYQGVDEBELFKLQMYGKGMKDKPPT 60  
DB 33 NKELDPIQKFLDIREYKAKRLASGGPVDTGPEYQGVDEBELFKLQMYGKGMKDKPPT 92  
QY 61 FNFEDPKFEVLKDKPOS 76  
DB 93 FNFEDPKFEVLKDKPOS 108  
RESULT 7  
Q6NZ59 PRELIMINARY; PRT; 108 AA.  
AC Q6NZ59; 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE ATP synthase, H+ transporting, mitochondrial Fo complex, subunit F6,  
DE isoform a.  
GN Name=ATP5J;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange S.J.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzyzanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Director MGC Project;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC066310; AA066310.1; -.  
DR GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.  
DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.  
DR GO; GO:0046961; F:hydrogen-transporting ATPase activity; IEA.  
DR GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.  
DR InterPro; IPR008387; ATP synth\_F6.  
DR Pfam; PF05511; ATP-synt\_F6; 1\_F6.  
SQ SEQUENCE 108 AA; 12627 MW; EDD2CDDCF01A10F17 CRC64;  
Query Match 76.1%; Score 306; DB 2; Length 108;  
Best Local Similarity 72.4%; Pred. No. 2e-24;  
Matches 55; Conservative 11; Mismatches 10; Indels 0; Gaps 0;  
QY 1 NKELDPIQKFLDIREYKAKRLASGGPVDTGPEYQGVDEBELFKLQMYGKGMKDKPPT 60  
DB 33 NKELDPIQKFLDIREYKAKRLASGGPVDTGPEYQGVDEBELFKLQMYGKGMKDKPPT 92  
QY 61 FNFEDPKFEVLKDKPOS 76  
DB 93 FNFEDPKFEVLKDKPOS 108  
RESULT 8  
Q6PG55 PRELIMINARY; PRT; 107 AA.  
AC Q6PG55; 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE MGC68738 protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OC NCBI\_Taxid=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange S.J.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzyzanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative";  
RL Dev. Dyn. 225:384-391(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RA Klein S., Strausberg R.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC057213; AAH57213.1; -  
 DR GO: GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.  
 DR GO: GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.  
 DR GO: GO:0046961; F:hydrogen-transporting ATPase activity; IEA.  
 DR GO: GO:0015986; P:ATP synthesis coupled proton transport; IEA.  
 DR InterPro: IPR008387; ATP synth\_F6.  
 DR Pfam: PF05511; ATP-synt F6; 1.  
 DR SQUENCE 107 AA; 12359 MW; 0F2C5BD80E6F286 CRC64;

Query Match 60.8%; Score 241; DB 2; Length 107;  
 Best Local Similarity 61.8%; Pred. No. 1.3e-17;  
 Matches 42; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 2 KELDVPQKFLDKIRRYKAKRLASGSPVDTGPYQOEVDRELFXKQMGKGMKPEPT 61  
 DB 36 KELDVPQKFLDKIRRYKAKRLASGSPVDTGPYQOEVDRELFXKQMGKGMKPEPT 95  
 QY 62 NFEDPKPE 69  
 DB 96 KFEPEKPE 103

RESULT 9  
 Q68FJ1 PRELIMINARY; PRT; 107 AA.  
 AC 068FJ1  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE MG686324 protein.  
 GN Name=MG686324;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenoportidae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;  
 RX MEDLINE=22341133; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Straussberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative."  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;  
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant P., Prange C.,  
 RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,  
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Maira M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;  
 RA Klein S., Gerhard D.S.;

RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC079787; AAH79787.1; -  
 DR InterPro: IPR008387; ATP synth\_F6.  
 DR Pfam: PF05511; ATP-synt F6; 1.  
 DR SQUENCE 107 AA; 12384 MW; C6EBC7EF08B54B CRC64;

Query Match 59.2%; Score 238; DB 2; Length 107;  
 Best Local Similarity 61.8%; Pred. No. 2.8e-17;  
 Matches 42; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

QY 2 KELDVPQKFLDKIRRYKAKRLASGSPVDTGPYQOEVDRELFXKQMGKGMKPEPT 61  
 DB 36 KELDVPQKFLDKIRRYKAKRLASGSPVDTGPYQOEVDRELFXKQMGKGMKPEPT 95  
 QY 62 NFEDPKPE 69  
 DB 96 KFEPEKPE 103

RESULT 10  
 Q6N7F7 PRELIMINARY; PRT; 112 AA.  
 AC 06N7F7  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Zgc:77541.  
 GN ORFNames=zgc:77541;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant P., Prange C.,  
 RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,  
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Maira M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;  
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant P., Prange C.,  
 RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,  
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Maira M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;  
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant P., Prange C.,  
 RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,  
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Maira M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.

Query Match 49.3%; Score 198; DB 2; Length 112;



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Best Local Similarity 56.5%; Pred. No. 4,7e-13;
Matches 35; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 2 KELDPVOKLFLDKIREYKAKRLASGSPVDGPEYQOEVDRELFLKQMYGKMGENDKRPPT 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 37 KQMDPIQKLFUDKIRDNYSKASGAVDAGPVQKNLAERTYKQRYGGGDLSPQPF 96

QY 62 NF 63
   ||
Db 97 SF 98

RESULT 11
QY 0707P4 PRELIMINARY; PRT; 117 AA.
AC 0707P4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ACP445 (Fragment).
GN Name=agCG56939; ORFNames=ENSNANG0000019097;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pezomyzeta;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelinae.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RL Anopheles Genome Sequencing Consortium;
RA Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
   EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
   preliminary data.
DR EMBL; AAB0108952; EAA10598.1; -
DR GO; GO:0016469; C:Proton-transporting two-sector ATPase complex; IEA.
DR GO; GO:0046933; F:Hydrogen-transporting ATP synthase activity. .; IEA.
DR GO; GO:0046961; F:Hydrogen-transporting ATPase activity. rota. .; IEA.
DR GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.
DR InterPro: IPR008387; ATP_synth_F6.
DR Pfam: PF05511; ATP_synth_F6.
FT NON TER 1
SQ SEQUENCE 117 AA; 12984 MW; 98DASB5F9376E95 CRC64;

Query Match 40.3%; Score 162; DB 2; Length 117;
Best Local Similarity 44.0%; Pred. No. 3e-09;
Matches 33; Conservative 16; Mismatches 22; Indels 4; Gaps 2;

QY 2 KELDPVOKLFLDKIREYKAKRLASGSPVDGPEYQOEVDRELFLKQMYGKMGENDK 57
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 40 KASPIQQLFVTKLREYAKQSGAGKLVDAIPEIQRELKQEMKAKQYGGGGEVDYTA 99

QY 58 PPTNFEDPKFEVD 72
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Db 100 FPAKFEEPKDIPIN 114

RESULT 12
QY 024407; O9VCN0;
AC 024407; O9VCN0;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE ATP synthase coupling factor 6, mitochondrial precursor (EC 3.6.3.14)
   (F6).
GN Name=ATP6yn-Cf6; ORFNames=CG4412;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pezomyzeta;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Ovary;
RX MEDLINE=99168769; PubMed=10071211; DOI=10.1007/s004380050942;
RA Casagrande C., Ragone G., Perrini B., Moschetti R., De Pinto V.,
RA Catizzi R., Barsanti P.;
RT "Identification of nuclear genes encoding mitochondrial proteins:
RT isolation of a collection of D. melanogaster cDNAs homologous to
RT sequences in the Human Gene index database."
RL Mol. Genet. 261:64-70(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer V.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hosteln D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaisli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lei Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclob J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [3]
RP GENOME REANNOTATION.
RX MEDLINE=22426069; PubMed=12537572;
RA Miara S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy U.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Belencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
CC -1- FUNCTION: This is one of the chains of the nonenzymatic component
CC (CF(0) subunit) of the mitochondrial ATPase complex. F6 seems to
CC be part of the stalk that links CF(0) to CF(1).
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -1- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic
CC core - and CF(0) - the membrane proton channel. CF(0) seems to
CC have nine subunits: a, b, c, d, e, f, g, f6 and 8 (or A6L).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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QY 62 NFED--BKFEVLDKPKQS 76  
DB 85 KLPDIDIDIPISVDLPEN 102

RESULT 14

Q812D0 PRELIMINARY; PRT; 54 AA.  
AC Q812D0;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
DE ATP synthase coupling factor VI (fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=15199140; DOI=10.1128/MCB.24.13.5844-5849.2004;  
RA Risteovski S., O'Leary D.A., Thornell A.P., Owen M.J., Kolia I.,  
RA Hertzog P.J.;  
RT "The ETS Transcription Factor GABP(alpha) is Essential for Early  
RT Embryogenesis.";  
RL Mol. Cell. Biol. 24:5844-5849(2004).  
DR EMBL; AF346288; AAC27831.1; .  
DR GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.  
DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity; .; IEA.  
DR GO; GO:0046961; F:hydrogen-transporting ATPase activity; IEA.  
DR GO; GO:0015966; P:ATP synthesis coupled proton transport; IEA.  
DR InterPro; IPR008387; ATP\_synth\_F6.  
DR Pfam; PF05511; ATP-synt\_F6; 1.  
FT NON TER 54  
SQ SEQUENCE 54 AA; 6285 MW; 82BFF0707AA7A29C CRC64;

Query Match 26.4%; Score 106; DB 2; Length 54;  
Best Local Similarity 90.9%; Pred. No. 0.00099;  
Matches 20; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKEIDPVOKLFVDKIREYKAKR 22  
DB 33 NKEIDPVOKLFVDKIREYKSKR 54

RESULT 15

Q6R840 PRELIMINARY; PRT; 285 AA.  
AC Q6R840;  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE 770RFP009.  
OS Bacteriophage 77.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.  
OX NCBI\_TaxID=259901;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=14716317;  
RA Liu J., Dehbi M., Moock G., Arhin F., Bauda P., Bergeron D.,  
RA Callejo M., Ferretti V., Ha N., Kwan T., McCarty J., Srikanth R.,  
RA Williams D., Wu J.J., Gros P., Pelletier J., Dubow M.;  
RT "Anticribial drug discovery through bacteriophage genomics.";  
RT Nat. Biotechnol. 22:185-191(2004).  
DR EMBL; AY508466; AAR67881.1; .  
SQ SEQUENCE 285 AA; 32577 MW; 67798DFDE282AE16 CRC64;

Query Match 20.0%; Score 80.5; DB 2; Length 285;  
Best Local Similarity 30.6%; Pred. No. 3;  
Matches 26; Conservative 14; Mismatches 20; Indels 25; Gaps 4;

QY 4 LDPVOKLFVDKIREYKAKRLASGPVDTGPE-----YQGEVDRELKLT 46  
DB 1 MDPILKGIDIKIEG-----ASKGPVETFTSKTWELVFGKFLVYDVKYVQREVEFE--KF 53

QY 47 KQYKGEMDKPTNFEDPKREVL 71  
DB 54 KEQF-KKEISSVPKNNLQEPQSL 77

Search completed: April 4, 2005, 19:23:26  
Job time : 120.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 19:11:13 ; Search time 26 Seconds  
(without alignments)  
281.249 Million cell updates/sec

Title: US-09-831-951A-2

Perfect score: 402  
Sequence: 1 NKEUDPVKLFIDKIREYKA.....KFTFNEFDPKFEVLDPKQOS 76

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	402	100.0	108	2 UC1167	coupling factor 6
2	333	82.8	108	1 UJB06	coupling factor 6
3	329	81.8	76	2 S00212	coupling factor 6
4	315	78.4	108	2 J70563	coupling factor 6
5	77.5	19.3	578	2 S51379	probable phospho
6	74	18.4	143	2 A12057	hypothetical prote
7	73	18.2	15	2 P00444	coupling factor 6
8	72.5	18.0	858	2 T18946	probable phosphol
9	71.5	17.8	813	2 T25144	hypothetical prote
10	71	17.7	253	2 T12108	hypothetical prote
11	67	16.7	797	2 A70453	glutamate ammonia
12	66	16.4	497	2 A84641	hypothetical prote
13	65	16.2	257	2 G70453	indole-3-glycerol
14	65	16.2	443	1 D64584	heat shock protein
15	65	16.2	443	2 F71929	heat shock protein
16	64.5	16.0	285	2 J00448	CATG-binding facto
17	64.5	16.0	1940	1 A24922	myosin heavy chain
18	64.5	16.0	1940	1 S04090	myosin heavy chain
19	64	15.9	808	2 C72858	myosin heavy chain
20	63.5	15.8	244	2 T25970	Acort-66 protein -
21	63.5	15.8	486	2 T24334	hypothetical prote
22	63.5	15.8	557	2 A61256	myosin heavy chain
23	63.5	15.8	996	2 S71750	myosin heavy chain
24	63.5	15.8	1934	2 I48153	import intermediat
25	63.5	15.8	1935	1 A57102	myosin heavy chain
26	63.5	15.8	1938	1 S06005	myosin beta heavy
27	63.5	15.8	1938	1 S06005	myosin alpha heavy
28	63.5	15.8	1939	1 A46762	myosin alpha heavy
29	63.5	15.8	1939	2 I48175	myosin heavy chain

30	63	15.7	364	2 T00200	hypothetical prote
31	63	15.7	1613	2 G64488	reverse gyrase (in
32	62.5	15.5	129	2 T31904	hypothetical prote
33	62.5	15.5	302	2 S66751	single stranded D
34	62.5	15.5	353	1 S66750	single stranded D
35	62.5	15.5	761	2 E64449	hypothetical prote
36	62.5	15.5	1935	1 S06006	myosin beta heavy
37	62	15.4	259	2 D85088	protein R09F10.1 (
38	62	15.4	500	2 A73385	glutamy1-cRNA(gln)
39	62	15.4	1177	2 I64233	hypothetical prote
40	61.5	15.3	231	2 T32070	hypothetical prote
41	61.5	15.3	233	2 S70531	bbr2.11 protein pr
42	61.5	15.3	390	2 S65650	hypothetical 43.6K
43	61.5	15.3	390	2 B91291	hypothetical prote
44	61.5	15.3	390	2 D86132	hypothetical prote
45	61	15.2	450	2 A11259	signal recognition

## ALIGNMENTS

## RESULT 1

UC1167  
coupling factor 6 precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Oct-1992 #sequence revision 09-Oct-1992 #text\_change 09-Jul-2004  
C:Accession: UC1167, A35933, C44300, I52239, S23283  
R:Tracer, H.L.; Loh, Y.P.; Birch, N.P.  
Gene 116, 291-292, 1992  
A:Title: Rat mitochondrial coupling factor 6: molecular cloning of a cDNA encoding the  
A:Reference number: JC1167, MUID:92339904, PMID:1366054  
A:Accession: UC1167  
A:Molecule type: mRNA  
A:Residues: 1-108 <TR>  
A:Cross-references: UNIPROT:P21571, EMBL:X54510, NID:g14214, PID:CA38369.1, PID:G5995  
R:Hiiguti, T.; Osaka, F.; Yoshinara, Y.; Tsutsumi, C.; Kawamura, Y.; Tan, I.; Toda, H.;  
Biochem. Biophys. Res. Commun. 171, 1079-1086, 1990  
A:Title: cDNA cloning and sequencing for the import precursor of coupling factor 6 in f  
A:Reference number: A55933, MUID:91024964, PMID:2145831  
A:Accession: A55933  
A:Molecule type: mRNA  
A:Residues: 1-108 <TR>  
A:Cross-references: GB:M73030, NID:G203529, PID:AAA40954.1, PID:G203530  
A>Note: part of this sequence, including the amino end of the mature protein, was deter  
R:Hiiguti, T.; Yoshinara, Y.; Kuroiwa, K.; Kawamura, Y.; Toda, H.; Sakiyama, F.  
J. Biol. Chem. 267, 22658-22661, 1992  
A:Title: A simple, rapid method for purification of epsilon-subunit, coupling factor 6,  
of epsilon-subunit.  
A:Reference number: A44300, MUID:93054567, PMID:1429613  
A:Accession: C44300  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 33-66 <HI2>  
A:Experimental source: liver  
A>Note: sequence extracted from NCBI backbone (NCBIP:119665)  
C:Comment: This is one of the soluble components required for coupling of phosphorylati  
C:Keywords: mitochondrion; oxidative phosphorylation  
C:Keywords: transit peptide (mitochondrion) #status predicted <TMP>  
F,33-108/Product: coupling factor 6 #status experimental <MAT>

Query Match	100.0%	Score 402,	DB 2,	Length 108;
Best Local Similarity	100.0%	Pred. No. 1.9e-36;		
Matches	76;	Conservative 0;	Mismatches 0;	Gaps 0;
Db	1	NKEUDPVKLFIDKIREYKASGGPVDTPGPEYQGVDELFKLKQMYGKGMXKPT	60	
Qy	33	NKEUDPVKLFIDKIREYKAKRLASGGPVDTPGPEYQGVDELFKLKQMYGKGMXKPT	92	
Db	61	FNFDPKFEVLDPKQOS 76		
Qy	93	FNFDPKFEVLDPKQOS 108		

## RESULT 2

JLB06

coupling factor 6 precursor, mitochondrial - bovine

N/Alternate names: ATP synthase coupling factor 6

C/Species: Bos primigenius taurus (cattle)

C/Date: 17-May-1995 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004

C/Accession: B27382; A03180; E39566

R/Walker, J.E.; Gay, N.J.; Powell, S.J.; Kostina, M.; Dyer, M.R.

A/Title: ATP synthase from bovine mitochondria: sequences of imported precursors of Olig

A/Reference number: A90527; MUID:88163536; PMID:2894843

A/Accession: B27382

A/Molecule type: mRNA

A/Residues: 1-108 &lt;MAL&gt;

A/Cross-references: UNIPROT:P02721; GB:M1921; NID:G163035; PIDN:AAA30511.1; PID:G163036

R/Fang, J.; Jacob, J.W.; Kemmer, B.I.; Recker, E.; Bradshaw, R.A.

Proc. Natl. Acad. Sci. U.S.A. 81, 6603-6607, 1984

A/Title: Amino acid sequence of bovine heart coupling factor 6.

A/Reference number: A03180; MUID:85038563; PMID:6149548

A/Accession: A03180

A/Molecule type: protein

A/Residues: 33-93; P, 95-108 &lt;FAN&gt;

A/Experimental source: heart

R/Walker, J.E.; Lutter, R.; Dupuis, A.; Runswick, M.J.

Biochemistry 30, 5369-5378, 1991

A/Title: Identification of the subunits of F<sub>1</sub>-F<sub>0</sub>-ATPase from bovine heart mitochondria.

A/Reference number: A39566; MUID:9124449; PMID:1827992

A/Accession: E39566

A/Molecule type: protein

A/Residues: 33-37 &lt;MA2&gt;

C/Comment: This is one of the soluble components required for coupling of phosphorylation

C/Superfamily: coupling factor 6

C/Keywords: mitochondrial; oxidative phosphorylation

F<sub>1</sub>-F<sub>32</sub>/Domain: transist peptide (mitochondrion) #status predicted <TMP>F<sub>33</sub>-108/Product: coupling factor 6 #status experimental <MAT>

Query Match 82.8%; Score 333; DB 1; Length 108;

Best Local Similarity 78.9%; Pred. No. 5.5e-29;

Matches 60; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 NKEIDPVQKFLDKIRRYKAKRLASGGPVDTPGPEYQOEVDRELFLKQMYGKGMDEKPT 60

DB 33 NKEIDPVQKFLVDKIRRYKAKRLASGGPVDAGPEYQODLDELFLKQMYGKGMDEKPT 92

QY 61 FNEEDPKFEVLDPKPOS 76

DB 93 FTEDPKFEVEKPOS 108

RESULT 3

S00212

coupling factor 6, mitochondrial - pig

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004

C/Accession: S00212

R/Chen, Z.W.; Mutt, V.; Barros-Sooderling, J.; Joernvall, H.

FEBS Lett. 226, 43-46, 1987

A/Title: Isolation and structural characterization of porcine coupling factor 6 from int

A/Reference number: S00212; MUID:8808364; PMID:2961617

A/Accession: S00212

A/Molecule type: protein

A/Residues: 1-76 &lt;CHE&gt;

A/Cross-references: UNIPROT:P13618

C/Superfamily: coupling factor 6

C/Keywords: mitochondrial; oxidative phosphorylation

Query Match 81.8%; Score 329; DB 2; Length 76;

Best Local Similarity 77.6%; Pred. No. 9.9e-29;

Matches 59; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 NKEIDPVQKFLDKIRRYKAKRLASGGPVDTPGPEYQOEVDRELFLKQMYGKGMDEKPT 60

DB 33 NKEIDPVQKFLVDKIRRYKAKRLASGGPVDAGPEYQODLDELFLKQMYGKGMDEKPT 92

DB 1 NKEIDPVQKFLVDKIRRYKAKRLASGGPVDAGPEYQODLDELFLKQMYGKGMDEKPT 60

QY 61 FNEEDPKFEVLDPKPOS 76

DB 61 FTEDPKFEVEKPOS 76

RESULT 4

JTB0563

coupling factor 6 precursor, mitochondrial - human

N/Alternate names: ATP synthase coupling factor 6

C/Species: Homo sapiens (man)

C/Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004

C/Accession: JTB0563; JQ1066; T14747

R/aved, A.A.; Ogata, K.; Sanadi, D.R.

Gene 97, 307-310, 1991

A/Title: Human mitochondrial ATP synthase: cloning cDNA for the nuclear-encoded precurs

A/Reference number: JTB0563; MUID:91153664; PMID:1825642

A/Accession: JTB0563

A/Molecule type: mRNA

A/Residues: 1-108 &lt;JAV&gt;

A/Cross-references: UNIPROT:P18859; GB:M37104; NID:G179274; PIDN:AAA51807.1; PID:G179274

A/Experimental source: fetal muscle

R/Higuti, T.; Tsurumi, C.; Kawamura, Y.; Teujita, H.; Osaka, F.; Yoshihara, Y.; Tani, I

Biochem. Biophys. Res. Commun. 178, 793-799, 1991

A/Title: Molecular cloning of cDNA for the import precursor of human coupling factor 6

A/Reference number: JQ1066; MUID:91315516; PMID:1830479

A/Accession: JQ1066

A/Molecule type: mRNA

A/Residues: 1-67, 'H', '69-108 &lt;HIG&gt;

A/Cross-references: GB:M73031; NID:G183785; PIDN:AAA8630.1; PID:G183786

A/Experimental source: kidney

R/Bium, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, August 1999

A/Reference number: Z18179

A/Accession: T14747

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-108 &lt;BLU&gt;

A/Cross-references: EMBL:AL110183

A/Experimental source: fetal kidney; clone DKFZ566A221

C/Genetics:

A/Gene: GDB:ATP5J

A/Cross-references: GDB:127519

A/Map position: 2pter-2qter

A/Note: DKFZ566A221.1

C/Superfamily: coupling factor 6

C/Keywords: mitochondrial; oxidative phosphorylation

F<sub>1</sub>-F<sub>32</sub>/Domain: transist peptide (mitochondrion) #status predicted <TPP>F<sub>33</sub>-108/Product: coupling factor 6 #status predicted <MAT>

Query Match 78.4%; Score 315; DB 2; Length 108;

Best Local Similarity 73.7%; Pred. No. 4.9e-27;

Matches 56; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 NKEIDPVQKFLDKIRRYKAKRLASGGPVDTPGPEYQOEVDRELFLKQMYGKGMDEKPT 60

DB 33 NKEIDPVQKFLVDKIRRYKAKRLASGGPVDASFEYQODLDELFLKQMYGKGMDEKPT 92

QY 61 FNEEDPKFEVLDPKPOS 76

DB 93 FNEEDPKFEVLDPKPOS 108

RESULT 5

S51379

probable phosphoesterase (EC 3.1.-.-) YJR361c [similarity] - yeast (Saccharomyces cerev

N/Alternate names: hypothetical protein I8039.13

C/Species: Saccharomyces cerevisiae

C/Date: 23-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 16-Aug-2004

C/Accession: S51379

R/Du, Z.

submitted to the EMBL Data Library, December 1994

A:Description: The sequence of *S. cerevisiae* com1d 8039.  
A:Reference number: S51377  
A:Accession: S51379  
A:Molecule type: DNA  
A:Residues: 1-578 <DUZ>  
A:Cross-references: UNIPROT:Q05924; EMBL:U19103; NID:g609404; PID:g609417; GSPDB:GN000122  
C:Comment: This sequence has motifs characteristic of a variety of phosphoesterases.  
C:Genetics:  
A:Gene: MIPS:YLR361C  
A:Cross-references: SGD:S0004353  
A:Map position: 12R  
C:Superfamily: phosphoesterase core homology  
C:Keywords: hydrolase  
F:249-339/Domain: phosphoesterase core homology <PEC>

Query Match 19.3%; Score 77.5; DB 2; Length 578;  
Best Local Similarity 33.3%; Pred. No. 1.7;  
Matches 30; Conservative 10; Mismatches 29; Indels 21; Gaps 6;

QY 7 VQLFL-LDKR---EYKARLASGPPVDTGEYQVDRLEFKLKQK---YKGE---54  
DB 206 LQKEPLVKKRYSEPAVLTKFVGTRPDTGAQRLQETDEGRKIVQLDLHLGVGESEC 265  
QY 55 MDKPTFN--EDPKFEV-----LDKQ 75  
DB 266 IDEYFKHACKADPKETTFVQVLDIERQ 295

RESULT 6  
AI2057  
hypotheetical protein alr2015 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Noc: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C:Accession: AI2057  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchihara, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AI2057  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-143 <KUR>  
A:Cross-references: UNIPROT:Q8YVG3; GB:BA000019; PIDN:BA87314.1; PID:G17131105; GSPDB:G  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr2015

Query Match 18.4%; Score 74; DB 2; Length 143;  
Best Local Similarity 30.8%; Pred. No. 0.78;  
Matches 28; Conservative 9; Mismatches 18; Indels 36; Gaps 6;

QY 5 DPL-QQLFLDKIRIRYKAKRLASGSPVDTGP-----EYQGVDRLEFKLKQYKGM 55  
DB 28 DPKQSTF-----YR-----ALGGVDPGETSLALKRFFOREIQAEILINIRYL---GCM 74  
QY 56 DKPTFN-----FEDPKFEVLD 72  
DB 75 ENLFTFNARKGHEHIIQLYQCDPADPKFQHLE 105

RESULT 7  
PD0444  
coupling factor 6 mitochondrial - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 05-Feb-1999  
C:Accession: PD0444  
R:Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.  
submitted to JIPID, August 1998  
A:Description: Proteome analysis of mouse brain.  
A:Reference number: PD0441  
A:Contents: Striatum

[illegible]

A:Map position: X  
A:introns: 93/1; 132/1; 170/1; 193/3; 209/1; 246/3; 345/3; 445/3; 490/3; 522/3; 593/1; 6

Query Match  
Best Local Similarity 17.8%; Score 71.5; DB 2; Length 813;  
Matches 19; Conservative 18; Mismatches 30; Indels 5; Gaps 3;

QY 1 NKEIDPVQKFLDKIREYKAKRLASGSPVDTGPEYQOEVDRELFLKQMGKGMDEKPT 60  
Db 744 HKEVFPPTNALILKIREYKQRMSTGSAE--PSIKPTIENITAIIDYK--PHENKLP 799  
QY 61 FNEDPKREVLD 72  
Db 800 SSFSS-STELID 810

RESULT 10  
T21008  
hypothetical protein F16B12.8 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T21008  
R:Alnscough, R.  
submitted to the EMBL Data Library, October 1996  
A:Reference number: Z19359  
A:Accession: T21008  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-253 <WII>  
A:Cross-references: UNIPROT:Q93516; EMBL:Z81064; PIDN:CAB02960.1; GSPDB:GNO0028; CESP:FL  
A:Experimental source: clone F16B12  
C:Genetics:  
A:Gene: CESP:F16B12.8  
A:Map position: X  
A:introns: 26/3; 63/3; 148/1

Query Match  
Best Local Similarity 17.7%; Score 71; DB 2; Length 253;  
Matches 19; Conservative 7; Mismatches 26; Indels 0; Gaps 0;

QY 1 NKEIDPVQKFLDKIREYKAKRLASGSPVDTGPEYQOEVDRELFLKQMGK 52  
Db 202 NMDLQYVMFMQFMDPKFKRLSDTFVAGAYSNRNDRDVKKYMFGK 253

RESULT 11  
A70453  
glutamate ammonia ligase adenyl-yl-transferase - *Aquifex aeolicus*  
C:Species: *Aquifex aeolicus*  
C>Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C:Accession: A70453  
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O  
V.  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.  
A:Reference number: A70300; MUID:98196666; PMID:9537320  
A:Accession: A70453  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-797 <AQP>  
A:Cross-references: UNIPROT:O67651; GB:AE000755; NID:g2984063; PIDN:AAC07604.1; PID:g298  
A:Experimental source: strain VFS  
C:Genetics:  
A:Gene: glne

Query Match  
Best Local Similarity 16.7%; Score 67; DB 2; Length 797;  
Matches 27; Conservative 8; Mismatches 25; Indels 16; Gaps 5;

QY 1 NKEIDPV-----QKFLDKIREYKAKRLASGSPVDTGPEYQOEVDRELFLKQMGK 53  
Db 553 NSDIDLVFAVKSLEK--EKVHE-KAKELVRLTAHTTGGLYSVD--FRLPMGSKG 605

QY 54 EMDKPTFNEDPKFE 69  
Db 606 EL-VPTFDYKXKFE 619

RESULT 12  
A84641  
hypothetical protein At2g24830 (imported) - *Arabidopsis thaliana*  
C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: A84641  
R:Lin, X.; Kaul, S.; Rounds, S.; Shee, T.P.; Bent, M.J.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon, L  
euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: A84641  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-497 <STO>  
A:Cross-references: UNIPROT:Q9SK49; GB:AE002093; NID:g4559368; PIDN:AAD23029.1; GSPDB:G  
A:Gene: At2g24830  
A:Map position: 2

Query Match  
Best Local Similarity 16.4%; Score 66; DB 2; Length 497;  
Matches 19; Conservative 11; Mismatches 23; Indels 8; Gaps 3;

QY 1 NKEIDPVQKFLDKIREYKAKRLASGSPVDTGP--FYQOEVD--DBELFLKQMGKGM 55  
Db 396 NEQIFPRH--EKHSESVKRNQKQSPVDRKALVEYQDEVRDLKEMLKLEQVNRNKK 452  
QY 56 D 56  
Db 453 D 453

RESULT 13  
G70453  
indole-3-glycerol phosphate synthase - *Aquifex aeolicus*  
C:Species: *Aquifex aeolicus*  
C>Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C:Accession: G70453  
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O  
V.  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.  
A:Reference number: A70300; MUID:98196666; PMID:9537320  
A:Accession: G70453  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-257 <AQP>  
A:Cross-references: UNIPROT:O67657; GB:AE000756; NID:g2984076; PIDN:AAC07616.1; PID:g29  
A:Experimental source: strain VFS  
C:Genetics:  
A:Gene: trpC  
C:Superfamily: indole-3-glycerol-phosphate synthase; trpC homology  
F/3-254/Domain: trpC homology <TRC>

Query Match  
Best Local Similarity 16.2%; Score 65; DB 2; Length 257;  
Matches 12; Conservative 12; Mismatches 10; Indels 6; Gaps 1;

QY 11 FLDKIREYKAKRLASGSPVDTGPEYQOEVDRELFLKQMG 50  
Db 3 FLEIVSYKESQ-----IDTSPEYLRKLELIBERKERY 36

RESULT 14  
D64584  
heat shock protein - *Helicobacter pylori* (strain 2695)



C.Species: Helicobacter pylori  
C.Date: 10-sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C.Accession: D64584  
R.Titomb, J.F., White, O., Kervatage, A.R., Clayton, R.A., Sutton, G.G., Fleischmann, R.D., Peterson, S., Loftus, B., Richardson, D., Dodson, R., Khairak, H.G., Glodek, A., McKennem, N., U.D., Kelley, J.M., Cotton, M.D., Weidman, J.M., Fujii, C., Bowman, C., Wathey, L., Nature 368, 539-547, 1997  
A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpik, P.D.; Smith, H.O.; Fraser, C.  
A.Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A.Reference number: A64520; PMID:97394467; PMID:9252185  
A.Accession: D64584  
A.Status: preliminary; nucleic acid sequence not shown; translation not shown  
A.Molecule type: DNA  
A.Residues: 1-443 <TOM>  
A.Cross-references: UNIPROT:O25254; GB:AEO00566; GI:AEO00511; NID:G2313628; PIDN:AD0075E8  
C.Superfamily: heat shock protein hslu; FESH/SECI8/CDC48-type ATP-binding domain homolog  
C.Keywords: nucleotide binding\_P-loop  
F:59-66/Region: nucleotide-binding motif A (P-loop)

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OM protein - protein search, using sw model

Run on: April 4, 2005, 18:46:29 ; Search time 30 Seconds  
(without alignments)  
189.111 Million cell updates/sec

Title: US-09-831-951A-2

Perfect score: 402  
Sequence: 1 NKEIDPVQKFLDKIREYKA.....KFTFNFDPKFEVLDKRQS 76

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTCUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	402	100.0	108	2	US-08-828-239-5
2	402	100.0	108	3	US-09-205-679-5
3	333	82.8	108	2	US-08-828-239-4
4	333	82.8	108	3	US-09-205-679-4
5	315	78.4	108	4	US-09-513-999C-8086
6	315	78.4	108	4	US-09-949-016-11049
7	310	77.1	108	2	US-08-828-239-3
8	310	77.1	108	3	US-09-205-679-3
9	309	76.9	106	4	US-09-513-999C-5967
10	252	62.7	114	2	US-08-828-239-1
11	252	62.7	114	3	US-09-205-679-1
12	156	38.8	69	4	US-09-513-999C-5968
13	67	16.7	583	4	US-09-489-039A-7653
14	64.5	16.0	1940	4	US-09-538-092-901
15	64.5	16.0	1940	4	US-09-949-016-8888
16	63.5	15.8	460	4	US-09-438-917-11
17	63.5	15.8	1118	4	US-09-949-016-6596
18	63.5	15.8	1120	4	US-09-949-016-10404
19	63.5	15.8	1886	4	US-08-938-105-3
20	63.5	15.8	1935	4	US-09-538-092-916
21	63.5	15.8	1939	3	US-09-310-187A-1
22	63.5	15.8	1939	4	US-09-538-092-917
23	63.5	15.8	1944	4	US-09-949-016-10929
24	63	15.7	351	4	US-09-489-039A-7442
25	62.5	15.5	606	4	US-09-252-991A-17409
26	62	15.4	539	4	US-09-248-796A-16770
27	61.5	15.3	290	4	US-09-107-433-3900

28	61.5	15.3	420	4	US-09-489-039A-8961	Sequence 8961, Ap
29	61	15.2	98	4	US-09-270-767-36028	Sequence 36028, A
30	61	15.2	98	4	US-09-270-767-51245	Sequence 51245, A
31	61	15.2	765	4	US-09-538-092-1340	Sequence 1340, Ap
32	60.5	15.0	555	4	US-09-543-681A-7166	Sequence 7166, Ap
33	60.5	15.0	1937	4	US-09-538-092-918	Sequence 918, App
34	60	14.9	392	4	US-09-198-452A-933	Sequence 933, App
35	60	14.9	507	4	US-09-949-016-11504	Sequence 11504, A
36	60	14.9	688	4	US-09-438-185A-870	Sequence 870, App
37	59.5	14.8	106	4	US-09-107-532A-5357	Sequence 5357, App
38	59.5	14.8	167	4	US-09-270-767-62466	Sequence 62466, A
39	59.5	14.8	454	4	US-09-270-767-46837	Sequence 46837, A
40	59.5	14.8	473	4	US-09-328-352-4658	Sequence 4658, Ap
41	59.5	14.8	690	4	US-09-489-039A-11040	Sequence 11040, A
42	59.5	14.8	970	2	US-08-449-645A-11	Sequence 11, App1
43	59.5	14.8	970	2	US-08-702-367A-11	Sequence 11, App1
44	59.5	14.8	970	5	PCT-US95-04681-11	Sequence 11, App1
45	59.5	14.8	994	3	US-08-542-635-2	Sequence 2, App11

#### ALIGNMENTS

RESULT 1  
US-08-828-239-5  
; Sequence 5, Application US/08828239  
; Patent No. 5849527  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: NOVEL ATP SYNTHASE COUPLING FACTOR 6  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/828,239  
; FILING DATE: Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PR-0260 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 108 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: Genbank  
; CLONE: 203530  
; US-08-828-239-5  
Query Match 100.0%; Score 402; DB 2; Length 108;  
Best Local Similarity 100.0%; Pred. No. 1,6e-43;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKELDPVOKLFLDKIREYKAKRLASGGPVDGTGPEYQOEVDRELFLKLKOMYGGKGMDEKFPPT 60  
Db 33 NKELDPVOKLFLDKIREYKAKRLASGGPVDGTGPEYQOEVDRELFLKLKOMYGGKGMDEKFPPT 92  
QY 61 FNFEDPKFEVLDKPOS 76  
Db 93 FNFEDPKFEVLDKPOS 108

## RESULT 2

US-09-205-679-5  
Sequence 5, Application US/09205679  
Patent No. 6048718  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Shah, Puri  
TITLE OF INVENTION: NOVEL ATP SYNTHASE COUPLING FACTOR 6  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/205,679  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/828,239  
FILING DATE: 03/31/1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0260 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: Genbank  
CLONE: 203530  
US-09-205-679-5

Query Match 100.0%; Score 402; DB 3; length 108;

Best Local Similarity 100.0%; Pred. No.1.6e-43;

Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKELDPVOKLFLDKIREYKAKRLASGGPVDGTGPEYQOEVDRELFLKLKOMYGGKGMDEKFPPT 60  
Db 33 NKELDPVOKLFLDKIREYKAKRLASGGPVDGTGPEYQOEVDRELFLKLKOMYGGKGMDEKFPPT 92  
QY 61 FNFEDPKFEVLDKPOS 76  
Db 93 FNFEDPKFEVLDKPOS 108

## RESULT 3

US-08-828-239-4  
Sequence 4, Application US/08828239

Patent No. 5849527  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Shah, Puri  
TITLE OF INVENTION: NOVEL ATP SYNTHASE COUPLING FACTOR 6  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/828,239  
FILING DATE: Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0260 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: Genbank  
CLONE: 625323  
US-08-828-239-4

Query Match 82.8%; Score 333; DB 2; length 108;

Best Local Similarity 78.9%; Pred. No.9.2e-35;

Matches 60; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 NKELDPVOKLFLDKIREYKAKRLASGGPVDGTGPEYQOEVDRELFLKLKOMYGGKGMDEKFPPT 60  
Db 33 NKELDPVOKLFLDKIREYKAKRLASGGPVDGTGPEYQOEVDRELFLKLKOMYGGKGMDEKFPPT 92  
QY 61 FNFEDPKFEVLDKPOS 76  
Db 93 FNFEDPKFEVLDKPOS 108

## RESULT 4

US-09-205-679-4

Sequence 4, Application US/09205679

Patent No. 6048718

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Shah, Puri

TITLE OF INVENTION: NOVEL ATP SYNTHASE COUPLING FACTOR 6

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/205,679
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,239
FILING DATE: 03/31/1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0260 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 625323
US-09-205-679-4

```

```

Query March 82.8%; Score 333; DB 3; Length 108;
Best Local Similarity 78.9%; Pred. No. 9.2e-35;
Matches 60; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 NKEIDPVQKFLDKIREYKAKRLASGGPVDTPGPEYQOEVDRELFLKQMYGKGEMDKFPT 60
Db 33 NKEIDPVQKFLVDKIREYKAKRLASGGPVDAGPEYQOGLDRELFLKQMYGKAMNTPFN 92

QY 61 FNEDPKFEVLDKPOS 76
Db 93 FTFEDPKFEVLEKPOS 108

```

```

RESULT 5
US-09-513-999C-8086
Sequence 8086, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Mline Edwards, J.B.
APPLICANT: Duclert, A.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59, US2, REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 8086
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
US-09-513-999C-8086

```

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Query March 78.4%; Score 315; DB 4; Length 108;
Best Local Similarity 73.7%; Pred. No. 1.8e-32;
Matches 56; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 NKEIDPVQKFLDKIREYKAKRLASGGPVDTPGPEYQOEVDRELFLKQMYGKGEMDKFPT 60
Db 33 NKEIDPVQKFLVDKIREYKAKRLASGGPVDAGPEYQOGLDRELFLKQMYGKAMNTPFN 92

```

```

Db 33 NKEIDPVQKFLVDKIREYKAKRLASGGPVDASSEYQOGLERELFLKQMGNAADMTFPT 92
QY 61 FNEDPKFEVLDKPOS 76
Db 93 FTFEDPKFEVLEKPOS 108

```

```

RESULT 6
US-09-949-016-11049
Sequence 11049, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C0001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11049
LENGTH: 108
TYPE: PRT
ORGANISM: Human
US-09-949-016-11049

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Query March 78.4%; Score 315; DB 4; Length 108;
Best Local Similarity 73.7%; Pred. No. 1.8e-32;
Matches 56; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 NKEIDPVQKFLDKIREYKAKRLASGGPVDTPGPEYQOEVDRELFLKQMYGKGEMDKFPT 60
Db 33 NKEIDPVQKFLVDKIREYKAKRLASGGPVDASSEYQOGLERELFLKQMGNAADMTFPT 92

QY 61 FNEDPKFEVLDKPOS 76
Db 93 FTFEDPKFEVLEKPOS 108

```

```

RESULT 7
US-08-828-239-3
Sequence 3, Application US/08828239
Patent No. 5849527
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: NOVEL ATP SYNTHASE COUPLING FACTOR 6
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,239
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

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;
; TYPE: amino acid
; STRANDEDNESS: single

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;          COMPUTER READABLE FORM:
;          MEDIUM TYPE: Diskette
;

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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828.239
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0260 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: 2496341
US-08-828-239-1
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Query Match 62.7%; Score 252; DB 2; Length 114;
Best Local Similarity 71.4%; Pred. No. 1.9e-24;
Matches 45; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
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Db 52 KIRYKSKRQTSGGPVDSSEYQOELRELFLKQMFNADMTPTFKFDPKFEVLEK 111
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```
QY 74 POS 76
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Db 112 PQA 114
```

```
RESULT 11
US-09-205-679-1
Sequence 1, Application US/09205679
Patent No. 6048718
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: NOVEL ATP SYNTHASE COUPLING FACTOR 6
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/205,679
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,239
FILING DATE: 03/31/1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
```

```
REFERENCE/DOCKET NUMBER: PF-0260 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Consensus
CLONE: 2496341
US-09-205-679-1
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Query Match 62.7%; Score 252; DB 3; Length 114;
Best Local Similarity 71.4%; Pred. No. 1.9e-24;
Matches 45; Conservative 9; Mismatches 9; Indels 0; Gaps 0;
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QY 14 KIRRYKAKRLASGGPVDTGPTGYQOEVDRELFLKQMTYKGMDFPTNFEDPKFEVLDK 73
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Db 52 KIRYKSKRQTSGGPVDSSEYQOELRELFLKQMFNADMTPTFKFDPKFEVLEK 111
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QY 74 POS 76
||:
Db 112 PQA 114
```

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RESULT 12
US-09-513-999C-5968
Sequence 5968, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PATENT NO. 6783961
FILE REFERENCE: 59,US2,REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 5968
LENGTH: 69
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 65
OTHER INFORMATION: Xaa-Pro or Ser
US-09-513-999C-5968
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Query Match 38.8%; Score 156; DB 4; Length 69;
Best Local Similarity 78.4%; Pred. No. 1.6e-12;
Matches 29; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
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RESULT 13
US-09-489-039A-7653
Sequence 7653, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
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Job time : 31 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: April 4, 2005, 18:55:50 ; Search time 94.5 Seconds  
(without alignments)  
266.678 Million cell updates/sec

Title: US-09-831-951A-2

Perfect score: 402

Sequence: 1 NKEIDPVQKFLDKIRREYKA.....KFFPFNPKREVLDKPKQS 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
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9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
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11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	358	89.1	108 17 US-10-926-543-77	Sequence 77, Appl
2	315	78.4	84 14 US-10-106-698-6594	Sequence 6594, Ap
3	315	78.4	108 11 US-10-111-410-119	Sequence 119, App
4	315	78.4	108 16 US-10-408-765A-1253	Sequence 1253, Ap
5	105	26.1	56 9 US-09-864-761-34125	Sequence 34125, A
6	105	26.1	56 9 US-09-864-761-34125	Sequence 34125, A
7	72.5	18.0	858 15 US-10-369-493-5537	Sequence 5537, Ap
8	72.5	18.0	858 15 US-10-369-493-5537	Sequence 5537, Ap
9	71.5	17.8	440 15 US-10-369-493-5537	Sequence 5537, Ap
10	70.5	17.5	262 14 US-10-156-761-11145	Sequence 11145, A
11	66.5	16.5	103 16 US-10-437-963-140910	Sequence 140910,
12	66.5	16.5	219 15 US-10-296-115-1011	Sequence 1011, Ap
13	66.5	16.5	458 14 US-10-213-181-14	Sequence 14, Appl

14	66.5	16.5	458 14 US-10-212-912-14	Sequence 14, Appl
15	66.5	16.5	458 14 US-10-213-044-14	Sequence 14, Appl
16	66.5	16.5	458 14 US-10-213-182-14	Sequence 14, Appl
17	66.5	16.5	458 14 US-10-213-060A-14	Sequence 14, Appl
18	66.5	16.5	458 14 US-10-213-052-14	Sequence 14, Appl
19	66.5	16.5	489 14 US-10-213-517-4	Sequence 4, Appl1
20	66.5	16.5	489 14 US-10-311-104-4	Sequence 4, Appl1
21	65	16.2	443 15 US-10-335-977-7965	Sequence 7965, Ap
22	65	16.2	448 15 US-10-335-977-7965	Sequence 7965, Ap
23	64.5	16.0	405 15 US-10-424-599-147941	Sequence 147941, Sequence 99, Appl
24	64.5	16.0	1940 16 US-10-408-765A-1175	Sequence 1175, Ap
25	64.5	16.0	1940 16 US-10-408-765A-1175	Sequence 1175, Ap
26	64	15.9	316 13 US-10-001-870-132	Sequence 132, App
27	64	15.9	320 15 US-10-424-599-256965	Sequence 256965, A
28	64	15.9	859 15 US-10-282-122A-65095	Sequence 65095, A
29	63.5	15.8	288 15 US-10-424-599-275777	Sequence 275777, Sequence 100, App
30	63.5	15.8	634 14 US-10-153-668-100	Sequence 104, App
31	63.5	15.8	1118 14 US-10-153-668-104	Sequence 104, App
32	63.5	15.8	1137 15 US-10-336-472-16	Sequence 16, Appl
33	63.5	15.8	1859 15 US-10-336-472-20	Sequence 20, Appl
34	63.5	15.8	1935 15 US-10-336-472-22	Sequence 22, Appl
35	63	15.7	458 15 US-10-369-493-5701	Sequence 3701, Ap
36	63	15.7	674 16 US-10-437-963-110667	Sequence 110667, Sequence 188046,
37	63	15.7	782 16 US-10-437-963-118046	Sequence 188046,
38	62.5	15.5	263 14 US-10-029-386-33579	Sequence 33579, A
39	62.5	15.5	485 16 US-10-408-765A-443	Sequence 443, App
40	62.5	15.5	794 14 US-10-128-714-3165	Sequence 3165, Ap
41	62.5	15.5	1138 14 US-10-128-714-8165	Sequence 8165, Ap
42	62.5	15.5	245 15 US-10-320-797-3350	Sequence 3350, Ap
43	62	15.4	1185 15 US-10-425-114-59597	Sequence 59597, A
44	62	15.4	259 15 US-10-369-493-6842	Sequence 6842, Ap
45	62	15.4	498 15 US-10-424-599-240937	Sequence 240937,

#### ALIGNMENTS

RESULT 1  
US-10-926-543-77 Application US/10926543  
; Sequence 77, Application US/10926543  
; Publication No. US20050048589A1  
; GENERAL INFORMATION:  
; APPLICANT: Jendoubi, Moncef  
; TITLE OF INVENTION: LUNG CANCER SPECIFIC GENE PRODUCTS: THEIR CODING SEQUENCE, THEIR  
; TITLE OF INVENTION: ANTIBODIES AND THEIR USE IN DIAGNOSTIC, THERAPEUTIC AND DISEASE  
; FILE REFERENCE: 705403.4004  
; CURRENT APPLICATION NUMBER: US/10/926,543  
; CURRENT FILING DATE: 2004-08-25  
; PRIOR APPLICATION NUMBER: US 60/497,790  
; PRIOR FILING DATE: 2003-08-25  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 77  
; LENGTH: 108  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-926-543-77

Query Match 89.1%; Score 358; DB 17; Length 108;  
Best local similarity 85.5%; Pred. No. 6e-35; 4; Indels 0; Gaps 0;  
Matches 65; Conservative 7; Mismatches

QY 1 NKEIDPVQKFLDKIRREYKARLASGGPVDTGPGYQGVNRELFKLQMYGKGMDEKPT 60  
DB 33 NKEIDPVQKFLVDKIRREYKSRQASGGVPDVGPEYQDLDRELYKLAQMGKGMDEPPT 92  
QY 61 FNEDPKREVLDKPKQS 76  
DB 93 FKFDPKREVLDKPKQS 108  
RESULT 2



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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33712
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000087.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
; OTHER INFORMATION: SWISSPROT HIT: P18859, EVALUATE 5.00e-24
; OTHER INFORMATION: EST_HUMAN HIT: AA128761.1, EVALUATE 5.00e-24
US-09-864-761-33712

Query Match      26.1%; Score 105; DB 9; Length 56;
Best Local Similarity 86.4%; Pred. No. 5.1e-05;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Cy      1 NKELDPVOKLFLDKIREYKAR 22
Db      35 NKELDPIOKLFLVDKIREYKSR 56

RESULT 6
US-09-864-761-34125
; Sequence 34125, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aegm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
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; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34125
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000139.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 5.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.5
; OTHER INFORMATION: EST_HUMAN HIT: AA128761.1, EVALUATE 5.00e-24
; OTHER INFORMATION: SWISSPROT HIT: P18859, EVALUATE 5.00e-24
US-09-864-761-34125

Query Match      26.1%; Score 105; DB 9; Length 56;
Best Local Similarity 86.4%; Pred. No. 5.1e-05;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Cy      1 NKELDPVOKLFLDKIREYKAR 22
Db      35 NKELDPIOKLFLVDKIREYKSR 56

RESULT 7
US-10-369-493-5536
; Sequence 5536, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
```

APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei

```

; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILING DATE: 2003-05-14
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 140910
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_42063C.1.pep
US-10-437-963-140910

Query Match
Best Local Similarity 30.0%; Pred. No. 4.4;
Matches 18; Conservative 12; Mismatches 23; Indels 7; Gaps 2;

Qy
6 PVQKLFIDKIRRYKAKRLASGSPVDTGPEYQOE-----FKLKQMTGKGMKPFPPN 62
Db
31 PLQNVFSPKVFYKAFNPFYFGLMEVPGYKKGVGKIKLRFKIK-----KGVQGFPPN 86

RESULT 12
US-10-236-115-1011
; Sequence 1011, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 1011
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-115-1011

Query Match
Best Local Similarity 23.6%; Pred. No. 11;
Matches 25; Conservative 10; Mismatches 32; Indels 39; Gaps 3;

Qy
4 LDPVQKLFIDKIRRYKAKRLASGSPVDTGPEYQOE-----VDRELFKLKQMTGK 53
Db
34 IDTWAMFTEB--DLDLVTLYFGSPDSTGHRYPESPERRRMVQVDRITGVYLRSTARN 91

Qy
54 -----EMDKPPTNFEDPKPEVLD 72
Db
92 HLTDRNLNLTSDHGMTTVDKRGADLVFHKFPNFTFDIFIELD 137

RESULT 13
US-10-213-181-14
; Sequence 14, Application US/10213181
; Publication No. US20030054484A1
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austen
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin
```

```

; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: P3133R1C7
; CURRENT APPLICATION NUMBER: US/10/213,181
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/052,594
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/177,118
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 14
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-213-181-14

Query Match
Best Local Similarity 23.6%; Pred. No. 28;
Matches 25; Conservative 10; Mismatches 32; Indels 39; Gaps 3;

Qy
4 LDPVQKLFIDKIRRYKAKRLASGSPVDTGPEYQOE-----VDRELFKLKQMTGK 53
Db
176 IDTWAMFTEB--DLDLVTLYFGSPDSTGHRYPESPERRRMVQVDRITGVYLRSTARN 233

Qy
54 -----EMDKPPTNFEDPKPEVLD 72
Db
234 HLTDRNLNLTSDHGMTTVDKRGADLVFHKFPNFTFDIFIELD 279

RESULT 14
US-10-212-912-14
; Sequence 14, Application US/10212912
; Publication No. US2003007737A1
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austen
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: P3133R1C2
; CURRENT APPLICATION NUMBER: US/10/212,912
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/052,594
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/172,059
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 14
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-212-912-14

Query Match
Best Local Similarity 16.5%; Score 66.5; DB 14; Length 458;
Matches 25; Conservative 10; Mismatches 32; Indels 39; Gaps 3;

Qy
4 LDPVQKLFIDKIRRYKAKRLASGSPVDTGPEYQOE-----VDRELFKLKQMTGK 53
Db
176 IDTWAMFTEB--DLDLVTLYFGSPDSTGHRYPESPERRRMVQVDRITGVYLRSTARN 233
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Qy 54 -----EMDKPTNFEDPKPEYLD 72  
Db 234 HLTDRNLNLTSDHGNTTVDRKAGDLVEFHKFPNFTFRDIEFFLD 279

## RESULT 15

US-10-213-044-14  
; Sequence 14, Application US/10213044  
; Publication No. US2003007738A1  
; GENERAL INFORMATION:  
; APPLICANT: Fong, Sherman  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune  
; TITLE OF INVENTION: Related Diseases  
; FILE REFERENCE: P3133R1C6  
; CURRENT APPLICATION NUMBER: US/10/213,044  
; CURRENT FILING DATE: 2002-08-05  
; PRIOR APPLICATION NUMBER: US 10/052,594  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: PCT/US00/30873  
; PRIOR FILING DATE: 2000-11-10  
; PRIOR APPLICATION NUMBER: US 60/177,118  
; PRIOR FILING DATE: 2000-01-20  
; NUMBER OF SEQ ID NOS: 24  
; SEQ ID NO 14  
; LENGTH: 458  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-213-044-14

Query Match 16.5%; Score 66.5; DB 14; Length 458;  
Best Local Similarity 23.6%; Pred. No. 28;  
Matches 25; Conservative 10; Mismatches 32; Indels 39; Gaps 3;

Qy 4 LDPVQKFLDKIREYKAKRLASGSPVDTGPEYQOE-----VDRELFKLQMYGKG 53  
Db 176 IDTWAMFTBE--DLDLVTLTFGEPSDSTGHRYPGSPERRRMVROVDRTVGYLRESIARN 233  
Qy 54 -----EMDKPTNFEDPKPEYLD 72  
Db 234 HLTDRNLNLTSDHGNTTVDRKAGDLVEFHKFPNFTFRDIEFFLD 279

Search completed: April 4, 2005, 19:15:11  
Job time : 103.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 18:58:20 ; Search time 124.5 Seconds

(without alignments)  
236.095 Million cell updates/sec

Title: US-09-831-951A-2

Perfect score: 402  
Sequence: 1 NKEADPVQKFLDKIREYKA.....KPTFNPEDPKFEVLDPKQFS 76

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	402	100.0	76	4	AAB80964 Rat Coupl
2	402	100.0	108	7	ADE63636 Rat Prote
3	402	100.0	108	7	ADE63632 Rat Prote
4	402	100.0	108	7	ADE63628 Rat Prote
5	402	100.0	108	7	ADE63624 Rat Prote
6	317	78.9	76	4	AAB80963 Human Cou
7	315	78.4	84	4	AAQ75820 Human col
8	315	78.4	108	2	AAV45888 Human bre
9	315	78.4	108	3	AAQ04005 Human sec
10	315	78.4	108	7	ADE63626 Human pro
11	315	78.4	108	7	ADE63638 Human pro
12	315	78.4	108	7	ADE63634 Human pro
13	315	78.4	108	7	ADE63630 Human pro
14	315	78.4	108	7	ADJ69447 Human hea
15	309	76.9	106	3	AAQ01886 Human sec
16	252	62.7	114	2	AAW87500 Human mit
17	252	62.7	114	3	AAV82605 Human mit
18	202	50.2	39	4	AAB80972 Rat CF6 P
19	156.5	38.9	106	3	ABB60627 Drosophil
20	156	38.8	69	3	AAQ01887 Human sec
21	132.5	33.0	147	4	ABB57878 Drosophil
22	105	26.1	20	4	AAB80968 Rat CF6 P
23	105	26.1	20	4	AAB80969 Rat CF6 P
24	105	26.1	56	4	AAAI3990 Peptide #
25	105	26.1	56	4	AAAI4420 Peptide #

ALIGNMENTS

RESULT 1	26	105	26.1	56	4	ABB33368 Peptide #
AAB80964	27	105	26.1	56	4	ABB32935 Peptide #
ID AAB80964 standard; protein; 76 AA.	28	105	26.1	56	4	AAAM26396 Peptide #
XX AAB80964;	29	105	26.1	56	4	AAAM26833 Peptide #
AC 08-JUN-2001 (first entry)	30	105	26.1	56	4	ABB27764 Human pep
XX	31	105	26.1	56	4	ABB28193 Human pep
DT	32	105	26.1	56	4	ABB18414 Protein #
XX	33	105	26.1	56	4	ABB18827 Protein #
DE	34	105	26.1	56	4	AAAM6547 Human bon
XX	35	105	26.1	56	4	AAAM66119 Human bon
XX	36	105	26.1	56	4	AAAM53736 Human bra
KW	37	105	26.1	56	4	AAAM54153 Human bra
KW	38	105	26.1	56	4	ABG47787 Human liv
KW	39	105	26.1	56	4	ABG48215 Human liv
KW	40	105	26.1	56	4	AAAM02147 Peptide #
DE	41	105	26.1	56	4	AAAM01731 Peptide #
XX	42	105	26.1	56	4	ABG35769 Human pep
XX	43	105	26.1	56	5	ABG36199 Human pep
XX	44	84	20.9	16	4	AAB80973 Rat CF6 P
XX	45	84	20.9	18	2	ADO24846 Human EBZ
03-AUG-2000; 2000WO-JP005210.						
17-SEP-1999; 99JP-00264687.						
(SUNR ) SUNTORY LTD.						
Oseanal T, Magoca K;						
WPI: 2001-266047/27.						
Coupling factor 6 useful in diagnosis of diseases relating to excess or lack of prostaglandin and cytoplasmic PLA2 activity in blood, and in screening drugs for treating e.g. cardiovascular infarction.						
Claim 15; Page 56-7; 70pp; Japanese.						
The present sequence is rat coupling factor 6 (CF6) protein. CF6 is a subunit of a proton-translocating ATPase found in mitochondria. CF6 can be used in diagnosis of diseases relating to excess or lack of prostaglandin and cytoplasmic PLA2 activity, and in screening inhibitors and potentiators as drugs to treat e.g. cardiovascular infarction, hypertension, arteriosclerosis, angina pectoris, cardiac insufficiency, cerebrovascular disorders, hyperlipemia, diabetes, bronchitis, gastric ulcer, pregnant eclampsia, haemolytic uremia syndrome, thrombopenic purpura, inflammatory diseases like cerebral infarction, acute pancreatitis, asthma, ARDS (adult respiratory distress syndrome), and						

CC rheumatoid arthritis  
XX Sequence 76 AA;  
SQ

Query Match 100.0%; Score 402; DB 4; Length 76;  
Best Local Similarity 100.0%; Pred. No. 2e-42;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKEIDPVQKFLDKIREYKAKRLASGGPVDTGPEYQOEVDRELFLKQWYKGMKMDKFPPT 60  
DB 1 NKEIDPVQKFLDKIREYKAKRLASGGPVDTGPEYQOEVDRELFLKQWYKGMKMDKFPPT 60

QY 61 FNFEDPKFEVLDPKQPS 76  
DB 61 FNFEDPKFEVLDPKQPS 76

RESULT 2  
ADE63636  
ID ADE63636 standard; protein; 108 AA.  
XX  
AC ADE63636;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Rat Protein P21571, SEQ ID NO 9580.  
XX  
KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX  
OS Rattus norvegicus.  
XX  
PN W02003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
DR WPI; 2003-268312/26.  
DR GENBANK; P21571.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 108 AA;  
XX

Query Match 100.0%; Score 402; DB 7; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.2e-42;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKEIDPVQKFLDKIREYKAKRLASGGPVDTGPEYQOEVDRELFLKQWYKGMKMDKFPPT 60  
DB 33 NKEIDPVQKFLDKIREYKAKRLASGGPVDTGPEYQOEVDRELFLKQWYKGMKMDKFPPT 92

QY 61 FNFEDPKFEVLDPKQPS 76  
DB 93 FNFEDPKFEVLDPKQPS 108

RESULT 3  
ADE63632  
ID ADE63632 standard; protein; 108 AA.  
XX  
AC ADE63632;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Rat Protein P21571, SEQ ID NO 9576.  
XX  
KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX  
OS Rattus norvegicus.  
XX  
PN W02003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
DR WPI; 2003-268312/26.  
DR GENBANK; P21571.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates



CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 108 AA;

Query Match 100.0%; Score 402; DB 7; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.2e-42;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NKEIDPVQKFLDKIREYKAKRLASGGPVDTGPEYQOEVDRELFLTKQMYGKGEMDKRPT 60  
DB 33 NKEIDPVQKFLDKIREYKAKRLASGGPVDTGPEYQOEVDRELFLTKQMYGKGEMDKRPT 92  
|||||  
|||||

OY 61 FNFEDEPKREVLDPKPOS 76  
DB 93 FNFEDEPKREVLDPKPOS 108  
|||||  
|||||

RESULT 4  
ADE63628  
ID ADE63628 standard; protein; 108 AA.

XX ADE63628;

XX 29-JAN-2004 (first entry)

XX Rat Protein P21571, SEQ ID NO 9572.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

XX Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GEHO ) GEN HOSPITAL CORP.

XX (FARB ) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; P21571.

XX New composition comprising two or more isolated polypeptides, useful for

XX preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat

XX or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 108 AA;

Query Match 100.0%; Score 402; DB 7; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.2e-42;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NKEIDPVQKFLDKIREYKAKRLASGGPVDTGPEYQOEVDRELFLTKQMYGKGEMDKRPT 60  
DB 33 NKEIDPVQKFLDKIREYKAKRLASGGPVDTGPEYQOEVDRELFLTKQMYGKGEMDKRPT 92  
|||||  
|||||

OY 61 FNFEDEPKREVLDPKPOS 76  
DB 93 FNFEDEPKREVLDPKPOS 108  
|||||  
|||||

RESULT 5  
ADE63624  
ID ADE63624 standard; protein; 108 AA.

XX ADE63624;

XX 29-JAN-2004 (first entry)

XX Rat Protein P21571, SEQ ID NO 9568.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

XX Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GEHO ) GEN HOSPITAL CORP.

XX (FARB ) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; P21571.

XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
XX  
PS Claim 1; Page: 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

SO Sequence 108 AA;

Query Match 100.0%; Score 402; DB 7; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.2e-42;  
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKELDPIQKFLDKIRRYKAKRLASGSPVDTGPGYQOEVDRELFLKQMTGKGMKPEPT 60  
DB 33 NKELDPIQKFLDKIRRYKAKRLASGSPVDTGPGYQOEVDRELFLKQMTGKGMKPEPT 92  
QY 61 FNEDPKFEVLDPKPOS 76  
DB 93 FNEDPKFEVLDPKPOS 108

RESULT 6  
AAB80963  
ID AAB80963 standard; protein; 76 AA.

AC AAB80963;

DT 08-JUN-2001 (first entry)

DE Human Coupling factor 6 CF6.

XX Human; coupling factor 6; CF6; antiinflammatory; antidiabetic; antilucer;  
XX cardiant; hypotensive; antispasmodic; antispasmodic;  
XX antispasmodic; proton-transporting ATPase; prostaglandin;  
XX cytoplasmic PLA 2; cardiovascular disorder; diabetes;  
XX inflammatory disorder; rheumatoid arthritis; cerebrovascular disorder.

OS Homo sapiens.

XX WO200121205-A1.

XX 29-MAR-2001.

PF 03-AUG-2000; 2000WO-JP005210.

PR 17-SEP-1999; 99JP-00264687.

PA (SUNR) SUNTORY LTD.

PI Oseana T, Magoca K;

DR WPI; 2001-266047/27.

PT Coupling factor 6 useful in diagnosis of diseases relating to excess or  
PT lack of prostaglandin and cytoplasmic PLA2 activity in blood, and in  
PT screening drugs for treating e.g. cardiovascular infarction.

PS Claim 15; Page 56; 70pp; Japanese.

CC The present sequence is human coupling factor 6 (CF6) protein. CF6 is a  
CC subunit of a proton-transporting ATPase found in mitochondria. CF6 can  
CC be used in diagnosis of diseases relating to excess or lack of  
CC prostaglandin and cytoplasmic PLA 2 activity, and in screening inhibitors  
CC and potentiators as drugs to treat e.g. cardiovascular infarction,  
CC hypertension, arteriosclerosis, angina pectoris, cardiac insufficiency,  
CC cerebrovascular disorders, hyperlipemia, diabetes, bronchitis, gastric  
CC ulcer, pregnant eclampsia, haemolytic uremia syndrome, thrombogenic  
CC purpura, inflammatory diseases like cerebral infarction, acute  
CC pancreatitis, asthma, ARDS (adult respiratory distress syndrome), and  
CC rheumatoid arthritis

SO Sequence 76 AA;

Query Match 78.9%; Score 317; DB 4; Length 76;  
Best Local Similarity 75.0%; Pred. No. 9.3e-32;  
Matches 57; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 NKELDPIQKFLDKIRRYKAKRLASGSPVDTGPGYQOEVDRELFLKQMTGKGMKPEPT 60  
DB 1 NKELDPIQKFLDKIRRYKAKRLASGSPVDTGPGYQOEVDRELFLKQMTGKGMKPEPT 60  
QY 61 FNEDPKFEVLDPKPOS 76  
DB 61 FNEDPKFEVLDPKPOS 76

RESULT 7  
AAG75820  
ID AAG75820 standard; protein; 84 AA.

AC AAG75820;

DT 03-SEP-2001 (first entry)

DE Human colon cancer antigen protein SEQ ID NO:6584.

XX Human; colon cancer; colon cancer antigen; diagnosis; detection;  
XX colorectal carcinoma; chromosome 10.

OS Homo sapiens.

PN WO200122920-A2.

PD 05-APR-2001.

PF 28-SEP-2000; 2000WO-US026524.

XX 29-SEP-1999; 99US-0157137P.

PR 03-NOV-1999; 99US-0163280P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Barash SC, Birse CE, Rosen CA;

DR WPI; 2001-235357/24.

XX N-PSDB; AAH35225.

PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,

PT useful for preventing, diagnosing and/or treating colorectal cancers.  
XX  
PS Claim 11; Page 8060-8062; 9803pp; English.

CC AAH32943 to AAH37195 and AAG75314 to AAG77788 represent human colon  
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the  
CC proteins are collectively known as colon cancer antigens. The colon  
CC cancer antigens have cytostatic activity and can be used in gene therapy  
CC and vaccine production. N and P may be used in the prevention, diagnosis  
CC and treatment of diseases associated with inappropriate P expression. For  
CC example, N and P may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of P by expressing inactive proteins or to  
CC supplement the patient's own production of P. Additionally, N may be used  
CC to produce the colon cancer-associated Ps by inserting the nucleic acids  
CC into a host cell and culturing the cell to express the proteins. N and P  
CC can be used in the prevention, diagnosis and treatment of colorectal  
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent  
CC sequences used in the exemplification of the present invention. N.B.  
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at  
CC time of publication, meaning no sequences are present for SEQ ID NO:1027  
CC to 1052, 7921 and 7922  
XX  
XQ Sequence 84 AA;

Query Match	78.4%	Score	315	DB	41	Length	84
Best Local Similarity	73.7%	Pred	No. 1.9e-31				
Matches	56	Conservative	11	Mismatches	9	Indels	0
						Gaps	0

```
QY      1 NKELDVQKLFUDKIREYKAKRLASGGPDTGPERYQGVNRELFTLKQMYTGKGMKPT 600
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      9 NKELPPIQLFVDKIREYKSKQTSGGPVDSSEYQELBRELFCLKQMGNADNMTPPT 688
```

```
QY      61 FNFEDPKFEVLDPQS 76
          |||||::|||:
Db      69 FKFEEDPKFEVIEKPQA 84
```

RESULT 8  
AAV48588  
ID AAV48588 standard; protein; 108 AA.

AC	AAAY48588;
XX	
DT	08-DEC-1999 (first entry)
...	

DE Human breast tumour-associated protein 49.  
XX  
KW Expressed sequence tag; EST; human; breast; cancer; gene therapy/

OS Homo sapiens.

PN DE19813839-A1.

PD 23-SEP-1999.

PF 20-MAR-1998; 98DE-01013839.  
YY

PR 20-MAR-1998; 98DE-01013839.  
XX

PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
XX

XX  
P1 specnt r, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosentahl A,  
XX

DR WFL; 1999-328981/43.  
DR N-PSDB; AA233657.

**PT Human nucleic acid sequences and protein products from tumor breast**

PT tissue, useful for breast cancer therapy.

PS Claim 22; 164; 188pp; German.

CC This invention describes novel human nucleic acid sequences from tumor  
CC breast tissue which have cytostatic activity. The nucleic acid sequences  
CC can be used to produce and isolate full-length gene sequences. They can  
CC be used to express proteins, which can be used as tools to find an  
CC actively against breast cancer. The sequences can be used in sense or  
CC antisense form. They are especially useful for medicaments for gene  
CC therapy to treat breast cancer. AAY8540-Y4861 represent protein  
CC fragments encoded by the expressed sequence tags described in the method  
CC of the invention  
CC  
CC  
CC  
CC Sequence 108 AA;  
SQ  
  
Query Match 78.4%; Score 315; DB 2; Length 108;  
Best Local Similarity 73.7%; Pred. No. 2.6e-31;  
Matches 56; Conservative 11; Mismatches 9; Indels 0; Gaps 0

[illegible]

RESULT 9  
AAG04005  
ID AAG04005 standard; protein; 108 AA

AC	AAG04005;
XX	
DT	06-OCT-2000 (first entry)

DE	Human secreted protein, SEQ ID NO: 8086.
XX	
KW	Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW	gene therapy; chromosome mapping.

OS	Homo sapiens.
XX	
PN	EP1033401-A2.

PD	06-SEP-2000.
XX	
PF	21-FEB-2000;

PR 26-FEB-1999; 99US-0122487P.  
XX  
PA (GEST ) GENSET.

XX	DATE	TIME	LOCATION	REMARKS
XX	10/10/20	10:00	1000000000	1000000000

DR N-PSDB; AAC04011.

PT New nucleic acid

PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

PS Claim 13; SEQ ID NO 8086; 71pp + Sequence Listing; English.  
 XY

CC The present sequence is a polypeptide encoded by one of a large number of  
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were

CC prepared from total human RNAs or polyA+ RNAs derived from 30 different

region (UR) of the mRNA because they are often obtained from oligo-d primed cDNA libraries. Such ESTs are not well suited for isolating cDNA

longer cDNA sequences have been obtained, the full 5' UTR is rarely

included. 5' ESTs are derived from mRNAs with intact 5' ends and can

CC are also used in diagnostic, forensic, gene therapy and chromosome

CC and to design expression and secretion vectors  
XX  
SQ Sequence 108 AA;  
Query Match 78.4%; Score 315; DB 3; Length 108;  
Best Local Similarity 73.7%; Pred. No. 2.6e-31;  
Matches 56; Conservative 11; Mismatches 9; Indels 0; Gaps 0;  
OY 1 NKEIDPVQKLFVDKIREYKAKRLASGSPVDGPEYQOEVDRELFLKMKMGKGMDFPT 60  
DB 33 NKEIDPIQKLFVDKIREYKSKRQTSQSPVDASSEYQOELERELFLKMKMGFNADMTFT 92  
OY 61 FNFEDPKFEVLDKPKQS 76  
DB 93 FKFEDEPKFEVLEKPKQA 108  
RESULT 10  
ADE63626  
ID ADE63626 standard; protein; 108 AA.  
AC ADE63626;  
XX  
XX 29-JAN-2004 (first entry)  
DT  
XX Human Protein P18859, SEQ ID NO 9570.  
DE  
XX Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KM spared nerve injury; SNI; Chung.  
XX Homo sapiens.  
OS  
XX WO2003016475-A2.  
FN  
XX 27-FEB-2003.  
PD  
XX 14-AUG-2002; 2002WO-US025765.  
PF  
XX 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
XX (GHEO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
XX Woolf C, D'urso D, Befort K, Costigan M;  
PI WPI; 2003-268312/26.  
DR GENBANK; P18859.  
DR  
XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
XX Claim 1; Page; 1017bp; English.  
PS  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating

CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 108 AA;  
Query Match 78.4%; Score 315; DB 7; Length 108;  
Best Local Similarity 73.7%; Pred. No. 2.6e-31;  
Matches 56; Conservative 11; Mismatches 9; Indels 0; Gaps 0;  
OY 1 NKEIDPVQKLFVDKIREYKAKRLASGSPVDGPEYQOEVDRELFLKMKMGKGMDFPT 60  
DB 33 NKEIDPIQKLFVDKIREYKSKRQTSQSPVDASSEYQOELERELFLKMKMGFNADMTFT 92  
OY 61 FNFEDPKFEVLDKPKQS 76  
DB 93 FKFEDEPKFEVLEKPKQA 108  
RESULT 11  
ADE63638  
ID ADE63638 standard; protein; 108 AA.  
XX  
XX ADE63638;  
AC  
XX 29-JAN-2004 (first entry)  
DT  
XX Human Protein P18859, SEQ ID NO 9582.  
DE  
XX Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KM spared nerve injury; SNI; Chung.  
XX  
XX Homo sapiens.  
OS  
XX WO2003016475-A2.  
FN  
XX 27-FEB-2003.  
PD  
XX 14-AUG-2002; 2002WO-US025765.  
PF  
XX 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
XX (GHEO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
XX Woolf C, D'urso D, Befort K, Costigan M;  
PI WPI; 2003-268312/26.  
DR GENBANK; P18859.  
DR  
XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
XX Claim 1; Page; 1017bp; English.  
PS  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity for identifying a compound or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 108 AA;

Query Match 78.4%; Score 315; DB 7; Length 108;  
Best Local Similarity 73.7%; Pred. No. 2.6e-31;  
Matches 56; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 NKEIDPVOKFLDKIRRYKAKRLASGGPVDTPGPEYQOEVDRELFLKQMYGKGMDEKPT 60  
Db 33 NKEIDPIQKLFVDKIRRYKSKRQTSGGPVDASSRYQOELELFLKQMPGNADMTFTPT 92

QY 61 FNFDPKFEVLDPKPOS 76  
Db 93 FKFDPKFEVLEKPOA 108

RESULT 12

ADE63634 ID ADE63634 standard; protein; 108 AA.

AC ADE63634;

DT 29-JAN-2004 (first entry)

DE Human Protein P18859, SEQ ID NO 9578.

KW Human; pain; neuronal tissue; gene therapy;  
KM spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

OS Homo sapiens.

PN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GEHO ) GEN HOSPITAL CORP.

PA (FARB ) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

DR WPI; 2003-268312/26.

DR GENBANK; P18859.

PT New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 108 AA;

Query Match 78.4%; Score 315; DB 7; Length 108;  
Best Local Similarity 73.7%; Pred. No. 2.6e-31;  
Matches 56; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 NKEIDPVOKFLDKIRRYKAKRLASGGPVDTPGPEYQOEVDRELFLKQMYGKGMDEKPT 60  
Db 33 NKEIDPIQKLFVDKIRRYKSKRQTSGGPVDASSRYQOELELFLKQMPGNADMTFTPT 92

QY 61 FNFDPKFEVLDPKPOS 76  
Db 93 FKFDPKFEVLEKPOA 108

RESULT 13

ADE63630 ID ADE63630 standard; protein; 108 AA.

AC ADE63630;

DT 29-JAN-2004 (first entry)

DE Human Protein P18859, SEQ ID NO 9574.

KW Human; pain; neuronal tissue; gene therapy;  
KM spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

OS Homo sapiens.

PN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GEHO ) GEN HOSPITAL CORP.

PA (FARB ) BAYER AG.



PD 06-SEP-2000.

PF 21-FEB-2000; 2000EP-00200610.

PR 26-FEB-1999; 99US-0122487P.  
XX

PA (GEST ) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

DR WPI; 2000-500381/45.

XX  
E

PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
PT diagnostic, forensic, gene therapy and chromosome mapping procedures

PS Claim 13; SEQ ID NO 5967; 71pp + Sequence Listing; English.

CC The present sequence is a polypeptide encoded by one of a large number of  
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were  
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different  
CC tissues. EST sequences usually correspond mainly to the 3' untranslated  
CC region (UTR) of the mRNA because they are often obtained from oligo-dT  
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA  
CC sequences derived from the 5' ends of mRNAs and even in those cases where  
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely  
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can  
CC therefore be used to obtain full length cDNAs and genomic DNA. 5' ESTs  
CC are also used in diagnostic, forensic, gene therapy and chromosome  
CC mapping procedures. They are used to obtain upstream regulatory sequences  
CC and to design expression and secretion vectors

**SD Sequence 106 AA;**

Query Match 76.9%; Score 309; DB 3; Length 106;

Matches 55; Conservative 10; Mismatches 9

QY 1 NKELDPVQKLFDKIREYKAKRLASGGPVDTGPEYQGEVDRELFKLKOMYGKGEMDKFPT 60

Db 33 NKELDPIQKLFVDKIREYKSKRQTSGGPVDASSEYQOELERELFKLKQMFGNADMTFPT 922

QY 61 FNFBDPKFEVLDP 74

Db 93 FKFE<sub>2</sub>DPKF<sub>2</sub>EV<sub>2</sub>IK<sub>2</sub>P 106

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 4, 2005, 18:59:30 ; Search time 118.5 Seconds  
(without alignments)  
328.422 Million cell updates/sec

Title: US-09-831-951A-1  
Perfect score: 394  
Sequence: 1 NKELDPIQKLFVDKIREYKS.....TFPTKPEDPKFEVLKRPQA 76

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	392	99.5	108	1	ATPR_HUMAN
2	383	97.2	108	2	Q6N259
3	363	92.1	108	2	Q8SPH6
4	346	87.8	108	1	ATPR_BOVIN
5	342	86.8	76	1	ATPR_PIG
6	332	84.3	108	1	ATPR_MOUSE
7	317	80.5	108	1	ATPR_RAT
8	245	62.2	107	2	Q68FJ1
9	237	60.2	107	2	Q6PG55
10	182	46.2	112	2	Q6NYF7
11	180	45.7	117	2	Q7Q7P4
12	154.5	39.2	106	1	ATPR_DROME
13	118	29.9	147	2	Q9VZ72
14	111	26.2	54	2	Q812D0
15	79.5	20.2	1934	2	Q75UE1
16	79.5	20.2	1940	1	MYH3_HUMAN
17	78.5	19.9	557	2	Q7M3B1
18	78	19.8	1103	2	Q64XS8
19	77.5	19.7	285	2	Q6R840
20	77.5	19.7	764	2	Q91411
21	76.5	19.4	891	2	Q90WH5
22	76.5	19.4	1931	2	Q910C5
23	76.5	19.4	1940	1	MYH3_RAT
24	75.5	19.2	372	2	Q6LIW9
25	75.5	19.2	611	2	Q14905
26	75.5	19.2	1491	2	Q75UB0
27	75.5	19.2	1931	2	Q91973
28	75.5	19.2	1934	1	MYH7_HUMAN
29	75.5	19.2	1935	1	MYH7_MESAU
30	75.5	19.2	1935	2	Q8MJJ9
31	75.5	19.2	1935	2	Q9BE39

32	75.5	19.2	1935	2	Q9GKR1	Q9GKR1 sus scrofa
33	75.5	19.2	1935	2	Q91283	Q91283 mus musculus
34	75.5	19.2	1938	1	MYH6_MOUSE	Q02566 mus musculus
35	75.5	19.2	1938	1	MYH6_RAT	P02563 ratus norv
36	75.5	19.2	1939	1	MYH6_HUMAN	P13533 homo sapien
37	75.5	19.2	1939	1	MYH6_MESAU	P13539 mesocricetu
38	73.5	18.7	1935	1	MYH7_RAT	Q02564 ratus norv
39	72.5	18.4	276	2	Q9D6G1	Q94691 mus musculus
40	72.5	18.4	285	1	ROAA_MOUSE	Q99020 mus musculus
41	72.5	18.4	285	2	Q9GX80	Q9GX80 ratus norv
42	72.5	18.4	298	2	Q9Z0U8	Q9Z0U8 ratus norv
43	72.5	18.4	311	2	Q80XR6	Q80XR6 mus musculus
44	72.5	18.4	331	2	Q883J1	Q883J1 ratus norv
45	72.5	18.4	332	2	Q9QX81	Q9QX81 ratus norv

## ALIGNMENTS

RESULT 1	ATPR_HUMAN	STANDARD	PRT	108 AA.
ID	ATPR_HUMAN	STANDARD	PRT	108 AA.
AC	P18859;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	ATP synthase coupling factor 6, mitochondrial precursor (EC 3.6.3.14) (Fe).			
GN	Name=ATP5F; Synonyms=ATPM;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91153664; PubMed=1825642; DOI=10.1016/0378-1119(91)90068-M;			
RA	Javed A.A., Ogata K., Sanadi D.R.;			
RT	"Human mitochondrial ATP synthase: cloning cDNA for the nuclear-			
RL	encoded precursor of coupling factor 6.";			
RL	Gene 97:307-310(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91315516; PubMed=1830479;			
RA	Higuchi T., Teuruni C., Kawamura Y., Tsujita H., Osaka F.;			
RT	Yoshikawa Y., Tani I., Tanaka K., Ichihara A.;			
RL	"Molecular cloning of cDNA for the import precursor of human coupling factor 6 of H(+)-ATP synthase in mitochondria.";			
RL	Biochem. Biophys. Res. Commun. 178:793-799(1991).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RX	MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;			
RA	Wismann S., Weil B., Wellenreuther R., Gassenhuber J., Glasel S.;			
RA	Ansorge W., Boecker M., Bloeker H., Bauerachs S., Blum H.;			
RA	Lauber J., Diesterhoef A., Beyer A., Koehler K., Strack N.;			
RA	Wendts H.-W., Ottenwelder B., Obermaier B., Tampe J., Heubner D.;			
RA	Mauheit R., Korn B., Klein M., Pouscka A.;			
RT	"Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs.";			
RL	Genome Res. 11:422-435(2001).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20285799; PubMed=10830953; DOI=10.1038/35012518;			
RA	Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.;			
RA	Park H.-S., Toyoda A., Ishii K., Tocoli Y., Choi D.-K., Soeda E.;			
RA	Oht M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.;			
RA	Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.;			
RA	Reichwald K., Rump A., Schillabel M., Schudy A., Zimmermann W.;			
RA	Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.;			
RA	Shintani A., Sasaki T., Nagamine K., Mitsuyma S., Antonarakis S.E.;			
RA	Mitsushima S., Shimizu N., Nordstiek G., Horzischer K., Brandt P.;			
RA	Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.;			
RA	Ramser J., Beck A., Klages S., Hennig S., Rieseemann L., Dargand E.;			

RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,  
 RA Leirach H., Reinhardt R., Yaspo M.-L.,  
 RT "The DNA sequence of human chromosome 21.",  
 RL Nature 405:311-319(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Eye;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loughlano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.",  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [6]  
 RP SEQUENCE OF 33-43.  
 RC TISSUE=Liver;  
 RX MEDLINE=93162045; PubMed=1286669;  
 RA Hochrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,  
 RA Pasquali C., Sanchez J.-C., Tisect J.-D., Bjelqvist B., Vargas R.,  
 RA Appel R.D., Hughes G.J.,  
 RT "Human liver protein map: a reference database established by  
 RT microsequencing and gel comparison.",  
 RL Electrophoresis 13:992-1001(1992).  
 CC -1- FUNCTION: This is one of the chains of the nonenzymatic component  
 CC (CF0) subunit of the mitochondrial ATPase complex. F6 seems to  
 CC be part of the stalk that links CF0 to CF1(1). Also involved in  
 CC the restoration of oligomycin-sensitive ATPase activity to  
 CC depleted F1-F0 complexes.  
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate +  
 CC H(+) (out).  
 CC -1- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic  
 CC core - and CF(0) - the membrane proton channel. CF(0) seems to  
 CC have nine subunits: a, b, c, d, e, f, g, F6 and 8 (or A6L).  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M37104; AAA51807.1; -;  
 DR EMBL: M73031; AAA58630.1; -;  
 DR EMBL: AL110183; CAB53667.1; -;  
 DR EMBL: AF001694; -; NOT ANNOTATED CDS.  
 DR EMBL: BC001178; AAH01178.1; -;  
 DR PIR: J70563; J70563.  
 DR SWISS-2DPAGE: P18859; HUMAN.  
 DR Genew: HGNC:847; ATP5J.  
 DR H-InvDB: HIX0016040; -;  
 DR Reactome: P18859; -;  
 DR MIM: 603152; -;  
 DR GO: GO:0005743; C:mitochondrial inner membrane; TAS.  
 DR GO: GO:0005739; C:mitochondrion; TAS.  
 DR InterPro: IPR008387; ATP synth\_F6.  
 DR Pfam: PF05511; ATP-synt\_F6; 1.  
 KW CF(0); Direct protein sequencing; Hydrogen ion transport;

KW Mitochondrion; Transic peptide.  
 FT TRANSIT 1 32 Mitochondrion.  
 FT CHAIN 33 108 ATP synthase coupling factor 6.  
 FT CONFLICT 68 68 Q -> H (in Ref. 2).  
 SQ SEQUENCE 108 AA; 12587 MW; EDC1A14F01A10F17 CRC64;  
 Query Match 99.5%; Score 392; DB 1; Length 108;  
 Best Local Similarity 98.7%; Pred. No. 1,1e-31;  
 Matches 75; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NKELDPIQKLFVDKIREYKSKRTSGSPYDASSEYOELERELFKLKMGFGNADNMTPT 60  
 DB 33 NKELDPIQKLFVDKIREYKSKRTSGSPYDASSEYOELERELFKLKMGFGNADNMTPT 92  
 QY 61 FKEDPKFVLEKPKA 76  
 DB 93 FKEDPKFVLEKPKA 108  
 RESULT 2  
 ID Q6NZ59 PRELIMINARY; PRT; 108 AA.  
 AC Q6NZ59;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6,  
 DE isoform a.  
 GN Name=ATP5J;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loughlano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcherfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.",  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX Direct MGC Project;  
 RA Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: BC066310; AAH66310.1; -;  
 DR GO: GO:0016669; C:proton-transporting two-sector ATPase complex; IEA.  
 DR GO: GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.  
 DR GO: GO:0046961; F:hydrogen-transporting ATPase activity, rota. ; IEA.  
 DR GO: GO:0015986; P:ATP synthesis coupled proton transport; IEA.  
 DR InterPro: IPR008387; ATP synth\_F6.  
 DR Pfam: PF05511; ATP-synt\_F6; 1.  
 SO SEQUENCE 108 AA; 12627 MW; EDD2C0CF01A10F17 CRC64;  
 Query Match 97.2%; Score 383; DB 2; Length 108;  
 Best Local Similarity 97.4%; Pred. No. 8.9e-31;

Matches	74;	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	
Qy	1	NKELDPIQKLPFDKIREYKSRQTSGGPVDASSEYQOELERELFTLKQMFQGNADNNTPT	60						
Db	33	NKELDPIQKLPFDKIREYKSRQTSGGPVDASSEYQOELERELFTLKQMFQGNADNNTFT	92						
Qy	61	KFEDPKFEVLEKPPA	76						
Db	93	KFEDPKFEVLEKPPA	108						
RESULT 3									
Q8SPH6		PRELIMINARY;	PRT;	108	AA.				
AC	Q8SPH6								
AD	Q8SPH6								
DT	01-JUN-2002	(TREMBLrel. 21, Created)							
DT	01-JUN-2002	(TREMBLrel. 21, Last sequence update)							
DT	01-OCT-2003	(TREMBLrel. 25, Last annotation update)							
DE	ATP synthase subunit F6.								
GN	Name=ATP5f;								
OC	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;								
OC	Cercopithecinae; Macaca.								
OX	NCBI_TaxId=9541;								
RA	[1]								
RA	SEQUENCE FROM N.A.								
RA	TISSUE=Brain parietal lobe;								
RA	Osada N., Kusuda J., Hirata M., Tanuma R., Hida M., Sugano S.,								
RA	Hirai M., Hashimoto K.;								
RT	"Search for genes positively selected during primate evolution by 5'-								
RT	end-sequence screening of cynomolgus monkey cDNAs."								
RL	Genomics 79:657-662(2002).								
DR	EMBL; AB072025; BAB86814.1; -								
DR	GO; GO:0016463; C:proton-transporting two-sector ATPase complex; IEA.								
DR	GO; GO:0046933; F:hydrogen-transporting ATP synthase activity. . .; IEA.								
DR	GO; GO:0046961; F:hydrogen-transporting ATPase activity, rota. . .; IEA.								
DR	GO; GO:0015986; F:ATP synthase coupled proton transport; IEA.								
DR	InterPro; IPR008387; ATP_synth_F6.								
DR	Pfam; PF05511; ATP-synt_F6; 1.								
DR	SEQUENCE 108 AA; 12587 MW; A13AC44891716C1E CRC64;								
Query Match 92.1%; Score 363; DB 2; Length 108;									
Best Local Similarity 89.5%; Pred. No. 9e-29;									
Matches 68; Conservative 3; Mismatches 5; Indels 0; Gaps 0;									
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Db	33	NKELDPIQKLPFDKIREYKSRQTSGGPVDGPEYQOELERELFTLKQMFQGNADNNTPT	92						
Qy	61	KFEDPKFEVLEKPPA	76						
Db	93	KFEDPKFEVLEKPPA	108						
RESULT 4									
ATPR_BOVIN		STANDARD;	PRT;	108	AA.				
AC	P02721;								
DT	21-JUL-1986	(Rel. 01, Created)							
DT	01-JAN-1990	(Rel. 13, Last sequence update)							
DT	05-JUN-2004	(Rel. 44, Last annotation update)							
DE	ATP synthase coupling factor 6, mitochondrial precursor (EC 3.6.3.14)								
GN	(F6).								
GN	Name=ATP5f;								
OS	Bos taurus (Bovine).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;								
OC	Bovinae; Bos.								
OX	NCBI_TaxId=9913;								
RA	[1]								
RA	SEQUENCE FROM N.A.								
RA	MEDLINE=88163536; PubMed=2894843;								

```

RA Walker J.E., Gay N.J., Powell S.J., Kostina M., Dyer M.R.:  

RT "ATP synthase from bovine mitochondria: sequences of imported  

RT precursors of oligomycin sensitivity conferral protein, factor 6, and  

RT adenosinetriphosphatase inhibitor protein.";  

RL Biochemistry 26:8613-8619(1987).  

RN [2]  

RP SEQUENCE OF 33-108.  

RX MEDLINE=85038563; PubMed=6149548;  

RA Fang J.-K., Jacobs J.W., Kanner B.I., Rackner R., Bradshaw R.A.:  

RT "Amino acid sequence of bovine heart coupling factor 6.";  

RL Proc. Natl. Acad. Sci. U.S.A. 81:6603-6607(1984).  

RN [3]  

RP SEQUENCE OF 33-37.  

RC TISSUE=Heart;  

RX MEDLINE=91242449; PubMed=1827992;  

RA Walker J.E., Lutter R., Dupuis A., Runswick M.J.:  

RT "Identification of the subunits of F1F0-ATPase from bovine heart  

RT mitochondria.";  

RL Biochemistry 30:5369-5378(1991).  

CC -I- FUNCTION: This is one of the chains of the nonenzymatic component  

CC (CF(0) subunit) of the mitochondrial ATPase complex. F6 seems to  

CC be part of the stalk that links CF(0) to CF(1). Also involved in  

CC the restoration of oligomycin-sensitive ATPase activity to  

CC depleted F1-F0 complexes.  

CC -I- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +  

CC H(+) (Out).  

CC -I- SUBUNIT: F-Type ATPases have 2 components, CF(1) - the catalytic  

CC core - and CF(0) - the membrane proton channel. CF(0) seems to  

CC have nine subunits: a, b, c, d, e, f, g, F6 and 8 (or A6L).  

CC  

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CC  

CC -----  

CC EMBL; M19217; AAA30511.1; -  

DR PIR; B27382; ULBO6.  

DR InterPro; IPR008187; ATP synth_F6.  

DR Pfam; PF05511; ATP-synt_F6; 1.  

DR CF(0); Direct protein sequencing; Hydrogen ion transport;  

KW Mitochondrion; Transit peptide.  

FT TRANSIT 1 32 Mitochondrion.  

FT CHAIN 33 108 ATP synthase coupling factor 6.  

FT FT 94 T -> F (in Ref. 2).  

FT FT 94 T -> F (in Ref. 2).  

SQ SEQUENCE 108 AA; 12532 MW; E5376A0518C3E1C8 CRC64;  

  

Query Match 87.8%; Score 346; DB 1; Length 108;  

Best Local Similarity 82.9%; Pred. No. 4,5e-27;  

Matches 63; Conservative 8; Mismatches 5; Indels 0; Gaps 0;  

  

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DB 33 NKEIDPIQKTFVDKIRFKSKRQTSQGPVDAAGEYQDDIRELFKIKOMYGKADMTPEPN 92  

OY 61 FKPEDPKFEVLEKPKQA 76  

DB 93 FTEDDPKFEVLEKPKQA 108  

  

RESULT 5  

AC ATPR_PIG STANDARD; PRT; 76 AA.  

ID P1618;  

DT 01-JAN-1990 (Rel. 13, Created)  

DT 01-JAN-1990 (Rel. 13, Last sequence update)  

DT 05-JUL-2004 (Rel. 44, Last annotation update)  

DE ATP synthase coupling factor 6, mitochondrial (EC 3.6.3.14) (F6).  

GN Name=ATP5F; (Pig).  

OS Sus scrofa (Pig).  

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP TISSUE=Intestine;  
 RX MEDLINE=8808363; PubMed=2961617; DOI=10.1016/0014-5793(87)80547-1;  
 RA Chen Z.-W., Mutt V., Barrios-Soderling J., Joernvall H.,  
 RT Evolution and structural characterization of porcine coupling factor  
 RL 6 from intestinal tissues.";  
 RT FEBS Lett. 226:43-46(1987).  
 CC -1- FUNCTION: This is one of the chains of the nonenzymatic component  
 CC (CF(0) subunit) of the mitochondrial ATPase complex. F6 seems to  
 CC be part of the stalk that links CF(0) to CF(1).  
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate +  
 CC H(+) (out).  
 CC -1- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic  
 CC core - and CF(0) - the membrane proton channel. CF(0) seems to  
 CC have nine subunits: a, b, c, d, e, f, g, F6 and 8 (or A6L).  
 DR PIR: S00212; S00212.  
 DR InterPro: IPR008387; ATP synth F6.  
 DR Pfam: PF05511; ATP-synth F6; 1.  
 KM CF(0). Direct protein sequencing; Hydrogen ion transport;  
 KM Mitochondrion.  
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 DB 1 NKEIDPIQKLFVDKIREYKSKQTSQGPVADSSSEYQGLERELFKLKGNGNDMTFTPT 60  
 QY 61 FKPEDPKFEVLEKPKQA 76  
 DB 61 FKPEDPKFEVLEKPKQA 76  
 DB 61 FKPEDPKFEVLEKPKQA 76  
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 AC P97450;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE ATP synthase coupling factor 6, mitochondrial precursor (EC 3.6.3.14)  
 DE (F6).  
 GN Name=Atp5j;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
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 RC STRAIN=C57BL/6;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
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 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,  
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 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustlich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lennard B., Lyons P.A.,  
 RA Meglert D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Perrea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,  
 RA Santoro R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Varrato R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilmink L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Maki K., Kawai T., Aizawa K., Arikawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,  
 RA Yemushi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Colon;  
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Tomihyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millhys S.J.,  
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
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 RA Villalon D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -1- FUNCTION: This is one of the chains of the nonenzymatic component  
 CC (CF(0) subunit) of the mitochondrial ATPase complex. F6 seems to  
 CC be part of the stalk that links CF(0) to CF(1).  
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate +  
 CC H(+) (out).  
 CC -1- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic  
 CC core - and CF(0) - the membrane proton channel. CF(0) seems to  
 CC have nine subunits: a, b, c, d, e, f, g, F6 and 8 (or A6L).  
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 CC  
 DR EMBL: U77128; AAB19213.1; -  
 DR EMBL: AK078484; BAC37301.1; -  
 DR EMBL: BC010766; AAH10766.1; -  
 DR SWISS-2DPAGE; P97450; MOUSE.  
 DR MGD: MGI:107777; Atp5j.  
 DR InterPro: IPR008387; ATP synth F6.  
 DR Pfam: PF05511; ATP-synth F6; 1.  
 KM CF(0); Hydrogen ion transport; Mitochondrion; Transit peptide.  
 FT TRANSIT 1 32  
 FT CHAIN 1 108  
 SQ SEQUENCE 108 AA; 12496 MW; E2A2B63F723CEBF CRC64;  
 Query Match 84.3%; Score 332; DB 1; Length 108;  
 Best Local Similarity 77.6%; Pred. No. 1.2e-25;  
 Matches 59; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 NKELDPIQKLFVDKIREYKSKRTSGGVPDASSEYQOELERELFKLKGMPGNADMTPT 60  
 DB 33 NKELDPIQKLFVDKIREYKSKRTSGGVPDASSEYQOELERELFKLKGMPGNADMTPT 92  
 QY 61 FKPEDPKFEVLEKPOA 76  
 DB 93 FKPEDPKFEVLEKPOA 108

RESULT 7  
 ATRP RAT STANDARD; PRT; 108 AA.  
 ID ATRP RAT STANDARD; PRT; 108 AA.  
 AC P21571;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE ATP synthase coupling factor 6, mitochondrial precursor (EC 3.6.3.14) (Fe).  
 GN Name=Atp5j;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=91024964; PubMed=2145831;  
 RA Higuti T., Osaka T., Yoshihara Y., Tsurumi C., Kawamura Y., Tani I., Toda H., Kakuno T., Sakiyama F., Tanaka K., Ichihara A.;  
 RT "cDNA cloning and precursor of the import precursor of coupling factor 6 in H(+) -ATP synthase from rat liver mitochondria.";  
 RL Biochem. Biophys. Res. Commun. 171:1079-1086(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Anterior pituitary;  
 RX MEDLINE=92339904; PubMed=1386054; DOI=10.1016/0378-1119(92)90528-W;  
 RA Tracer H.L., Loh Y.P., Birch N.P.;  
 RT "Rat mitochondrial coupling factor 6: molecular cloning of a cDNA encoding the imported precursor.";  
 RL Gene 116:291-292(1992).  
 RN [3]  
 RP SEQUENCE OF 33-66.  
 RC TISSUE=Liver;  
 RX MEDLINE=93054567; PubMed=1429613;  
 RA Higuti T., Yoshihara Y., Kuroiwa K., Kawamura Y., Toda H., Sakiyama F.;  
 RT "A simple, rapid method for purification of epsilon-subunit, coupling factor 6, subunit d, and subunit e from rat liver H(+)-ATP synthase and determination of the complete amino acid sequence of epsilon-subunit.";  
 RL J. Biol. Chem. 267:22658-22661(1992).  
 CC -1- FUNCTION: This is one of the chains of the nonenzymatic component (CF0) subunit of the mitochondrial ATPase complex. F6 seems to be part of the stalk that links CF0 to CF1).  
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate + H(+) (out).  
 CC -1- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic core - and CF(0) - the membrane proton channel. CF(0) seems to have nine subunits: a, b, c, d, e, f, g, F6 and 8 (or A6L).  
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 CC -----  
 CC EMBL: M73030; AAA0954.1; -;  
 CC DR EMBL: X54510; CAA38369.1; -;  
 CC DR PIR: JCI167; JCI167.  
 CC DR HSC-2DPAGE; P21571; RAT.

DR RGD; 621376; Atp5j.  
 DR InterPro: IPR008387; ATP synth\_F6.  
 DR Pfam: PF05511; ATP-synt\_F6; 1.  
 KM CF(0) ; Direct protein sequencing; Hydrogen ion transport;  
 FT Mitochondrion; Transit peptide.  
 FT TRANSIT 1 32  
 FT CHAIN 33 108  
 SQ SEQUENCE 108 AA; 12494 MW; F61177C9681B5F51 CRC64;

Query Match 80.5%; Score 317; DB 1; Length 108;  
 Best Local Similarity 75.0%; Pred. No. 3,7e-24;  
 Matches 57; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 NKELDPIQKLFVDKIREYKSKRTSGGVPDASSEYQOELERELFKLKGMPGNADMTPT 60  
 DB 33 NKELDPIQKLFVDKIREYKSKRTSGGVPDASSEYQOELERELFKLKGMPGNADMTPT 92  
 QY 61 FKPEDPKFEVLEKPOA 76  
 DB 93 FKPEDPKFEVLEKPOA 108

RESULT 8  
 ID 068FJ1 PRELIMINARY; PRT; 107 AA.  
 AC 068FJ1;  
 DT 25-OCT-2004 (Trembl) 28, Created)  
 DT 25-OCT-2004 (Trembl) 28, Last sequence update)  
 DT 25-OCT-2004 (Trembl) 28, Last annotation update)  
 DE MGC86324 protein.  
 GN Name=MGC86324;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus RT initiative.";  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heileh F., Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Feyhy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouford G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Kravinsky M.I., Skalek A.U., Smalhus D.E., Schnerch A., Schein J.B., Kravinsky M.I., Skalek A.U., Smalhus D.E., Schnerch A., Schein J.B., "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Klein S., Gerhard D.S.;

RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC079787; AAH79787.1; -.  
DR InterPro: IPR008387; ATP synth\_F6.  
DR Pfam: PF05511; ATP-synt\_F6; 1.  
SQ SEQUENCE 107 AA; 12384 MW; C6EBBC7EF08B854E CRC64;

Query Match 62.2%; Score 245; DB 2; Length 107;  
Best Local Similarity 61.8%; Pred. No. 6e-17;  
Matches 42; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 2 KEIDPIQKLFVDKIREYKSRQTSGGPVDAASSEYQOELEBELFKLQKMFNADMTPTPT 61  
DB 36 KEIDPIQKLFVDKIREYKSRQTSGGPVDAASSEYQOELEBELFKLQKMFNADMTPTPT 95

QY 62 KFEDEPKFE 69  
DB 96 KFEDEPKFE 103

## RESULT 9

ID Q6PG55 PRELIMINARY; PRT; 107 AA.  
AC Q6PG55;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE MG68738 protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
OC Xenopodidae; Xenopus.  
NCBI\_Taxid=8355;

RP SEQUENCE FROM N.A.  
RC TISSUE=Spine;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raba S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE FROM N.A.  
RC TISSUE=Spine;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strauberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative.";  
RL Dev. Dyn. 225:384-391(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spine;  
RA Klein S., Strauberg R.;  
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC057213; AAH57213.1; -.  
DR GO: GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.  
GO: GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.

DR GO: GO:0046961; F:hydrogen-transporting ATPase activity; rota. . .; IEA.  
DR GO: GO:0015986; P:ATP synthesis coupled proton transport; IEA.  
DR InterPro: IPR008387; ATP synth\_F6.  
DR Pfam: PF05511; ATP-synt\_F6; 1.  
SQ SEQUENCE 107 AA; 12359 MW; 0F2C5BD80E6F286 CRC64;

Query Match 60.2%; Score 237; DB 2; Length 107;  
Best Local Similarity 60.3%; Pred. No. 3.8e-16;  
Matches 41; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 2 KEIDPIQKLFVDKIREYKSRQTSGGPVDAASSEYQOELEBELFKLQKMFNADMTPTPT 61  
DB 36 KEIDPIQKLFVDKIREYKSRQTSGGPVDAASSEYQOELEBELFKLQKMFNADMTPTPT 95

QY 62 KFEDEPKFE 69  
DB 96 KFEDEPKFE 103

## RESULT 10

ID Q6NYF7 PRELIMINARY; PRT; 112 AA.  
AC Q6NYF7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Zgc:77541.  
GN ORFNames=zgc:77541.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
NCBI\_Taxid=7955;

RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raba S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RA Strauberg R.;  
RL Submitted (Feb-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC066613; AAH66613.1; -.  
DR ZFIN: ZDB-GENE-040426-2534; zgc:77541.  
DR GO: GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.  
DR GO: GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.  
DR GO: GO:0046961; F:hydrogen-transporting ATPase activity; rota. . .; IEA.  
DR InterPro: IPR008387; ATP synth\_F6.  
DR Pfam: PF05511; ATP-synt\_F6; 1.  
SQ SEQUENCE 112 AA; 12244 MW; 4DA7B791BDAP87D7 CRC64;  
Query Match 46.2%; Score 182; DB 2; Length 112;

```

Beet Local Similarity 53.2%; Pred. No. 1.3e-10;
Matches 33; Conservative 12; Mismatches 17; Indels 0; Gaps 0;

OY 2 KELDPIQKLFVDKIREYKSKRQTSQGPVDASSEYQOELERELFLKQKMGNDMMTPFP 61
Db 37 KDMBDIQKLFVDKIRDNYSKVSAGGVADGVPYKNIARETTKLRQLYGGGLSKPQF 96

OY 62 KF 63
Db 97 SF 98

RESULT 11
ID 0707P4 PRELIMINARY; PRT; 117 AA.
AC 0707P4;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE AGCP4445 (Fragment).
GN Name=agcG56939; ORFNames=ENSANG00000019097;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1 CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AA01008952; EAA10598.1;
DR GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.
DR GO; GO:0046961; F:hydrogen-transporting ATP synthase activity; IEA.
DR GO; GO:0015966; P:ATP synthetase coupled proton transport; IEA.
DR InterPro: IPR00387; ATP synth_F6.
DR Pfam; PF05511; ATP-synth_F6; 1.
FT NON_TER 1
SQ SEQUENCE 117 AA; 12984 MW; 98DA5B85F9376E95 CRC64;

Query Match 45.7%; Score 180; DB 2; Length 117;
Beet Local Similarity 51.4%; Pred. No. 2.2e-10;
Matches 37; Conservative 13; Mismatches 18; Indels 4; Gaps 2;

OY 2 KELDPIQKLFVDKIREYKSKRQTSQGP-VDSSEYQOELERELFLKQKMGNA---DMNT 57
Db 40 KASDPIQKLFVDKIREYKSKRQTSQGPVDATPELQRELKQKMGNAQYGGGGEEDMTA 99

OY 58 PPTKEFEDPKFE 69
Db 100 PPAKFEEPKID 111

RESULT 12
ID 0707P4 STANDAR; PRT; 106 AA.
AC 024407; QAVCNO;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 25-JAN-2005 (Rel. 46, Last annotation update)
DE ATP synthase coupling factor 6, mitochondrial precursor (EC 3.6.3.14)
DE (F6).
GN Name=ATPsyn-F6; ORFNames=CG4412;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC TISSUE=Ovary;
RX MEDLINE=99168769; PubMed=10071211; DOI=10.1007/s004380050942;
RA Caggese C., Ragone G., Perrini B., Moschetti R., De Pinto V.,
RA Cairati R., Barsanti P.;
RT "Identification of nuclear genes encoding mitochondrial proteins:
RT isolation of a collection of D. melanogaster cDNAs homologous to
RT sequences in the Human Gene Index database.";
RL Mol. Gen. Genet. 261:64-70(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoekling R.A., Galle R.F.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.D.,
RA Abiril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodeon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibergman C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Sidon-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler B., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye Y., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP GENOME REANNOTATION.
RX MEDLINE=22426069; PubMed=12537572;
RA Miara S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield B.O., Bayraktaroglu L., Bernik S.B.,
RA Betencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
CC -1- FUNCTION: This is one of the chains of the nonenzymatic component
CC (CF(0) subunit) of the mitochondrial ATPase complex. F6 seems to
CC be part of the stalk that links CF(0) to CF(1).
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -1- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic
CC core - and CF(0) - the membrane proton channel. CF(0) seems to
CC have nine subunits: a, b, c, d, e, f, g, F6 and 8 (or A6L).
CC CC
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 DR EMBL; X99665; CAA67979.1; -  
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 DR InfAct; Q24407; -  
 DR FlyBase; FBgn0016119; ATPsyn-*cf6*.  
 DR InterPro; IPR008387; ATP-synth\_F6.  
 DR Pfam; PF05511; ATP-synth\_F6; 1.  
 DR CF(0); Hydrogen ion transport; Mitochondrion; Transist peptide.  
 FT TRANSIT 1 ?  
 FT CHAIN ? 106 ATP synthase coupling factor 6.  
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Query Match 39.2%; Score 154.5; DB 1; Length 106;  
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 Matches 35; Conservative 19; Mismatches 19; Indels 7; Gaps 4;

QY 1 NKELDPIQKLVDPKIREYKSRQTSRSGP-VPASSEYQOELERELPKLKMPGN--ADNM 56  
 Db 29 NKASDPDQQLFLDKRREYKQK-SAGGKLVDSNPDIERELKELDRVAKQFSGDKTDM 86  
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 Db 87 KPFEPQFPDVKVPDITQAPQ 106

RESULT 13  
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 DT 01-MAY-2000 (TRENBLrel. 13. Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26. Last annotation update)  
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 GN ORENames=CGJ2027;  
 OS Drosophila melanogaster (Fruit fly).  
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 RX MEDLINE=22426103; PubMed=12537606;  
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [38]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426104; PubMed=12537607;  
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [39]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426105; PubMed=12537608;  
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [40]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426106; PubMed=12537609;  
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [41]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426107; PubMed=12537610;  
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [42]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426108; PubMed=12537611;  
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [43]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426109; PubMed=12537612;  
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [44]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426110; PubMed=12537613;  
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [45]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426111; PubMed=12537614;  
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [46]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426112; PubMed=12537615;  
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [47]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426113; PubMed=12537616;  
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [48]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426114; PubMed=12537617;  
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [49]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426115; PubMed=12537618;  
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [50]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426116; PubMed=12537619;  
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [51]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426117; PubMed=12537620;  
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [52]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426118; PubMed=12537621;  
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [53]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426119; PubMed=12537622;  
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [54]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=224



Qy 62 KFED 65  
 Db 85 KLPD 88

## RESULT 14

Q812D0 PRELIMINARY; PRT; 54 AA.  
 AC Q812D0;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)  
 DE ATP synthase coupling Factor VI (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed:15199140; DOI=10.1128/MCB.24.13.5844-5849.2004;  
 RA Risteveki S., O'Leary D.A., Thornell A.P., Owen M.J., Kola I.,  
 RA Hertzog P.J.;  
 RT "The ETS Transcription Factor GABP(alpha) Is Essential for Early  
 RT Embryogenesis.";  
 RL Mol. Cell. Biol. 24:5844-5849(2004).  
 DR EMBL; AF346288; AAC27831.1; -.  
 DR GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.  
 DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity; IEA.  
 DR GO; GO:0046961; F:hydrogen-transporting ATP synthase activity; IEA.  
 DR GO; GO:0015986; P:ATP synthesis coupled proton transport; IEA.  
 DR InterPro; IPR008387; ATP synth\_F6.  
 DR Pfam; PF05511; ATP-synt\_F6; 1.  
 DR NOW TER  
 SQ SEQUENCE 54 AA; 6285 MW; 82BFF0707AA7A29C CRC64;  
 Query Match 28.2%; Score 111; DB 2; Length 54;  
 Best Local Similarity 95.5%; Pred. No. 0.00077;  
 Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NKELDPIQKLFVDKIREYKSKR 22  
 Db 33 NKELDPIVQKLFVDKIREYKSKR 54

## RESULT 15

Q75UE1 PRELIMINARY; PRT; 1934 AA.  
 AC Q75UE1;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Myosin heavy chain.  
 GN Name=LjMyHc1;  
 OS Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
 OC Petromyzontiformes; Petromyzontidae; Leptocephala.  
 NCBI\_TaxID=94989;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kusakabe R., Takechi M., Tochinal S., Kuratani S.;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB126173; BABD1606.1; -.  
 DR HSSP; P24733; IKK7.  
 DR GO; GO:0016459; C:myosin; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0003774; F:motor activity; IEA.  
 DR InterPro; IPR000048; IQ\_region.  
 DR InterPro; IPR001609; Myosin\_head.  
 DR InterPro; IPR004009; Myosin\_N.  
 DR InterPro; IPR002928; Myosin\_tail.  
 DR Pfam; PF00063; Myosin\_head; 1.  
 DR Pfam; PF02736; Myosin\_N; 1.  
 DR Pfam; PF01576; Myosin\_tail\_1; 1.

DR PRINTS; PR00193; MYOSINHEAVY.  
 DR ProDom; PD000355; Myosin\_head; 1.  
 DR SMART; SM00242; MYSC; 1.  
 DR PROSITE; PS50096; IQ; 1.  
 SQ SEQUENCE 1934 AA; 222488 MW; 7D4261D4CB5F85DD CRC64;

Query Match 20.2%; Score 79.5; DB 2; Length 1934;  
 Best Local Similarity 31.8%; Pred. No. 57;  
 Matches 21; Conservative 13; Mismatches 31; Indels 1; Gaps 1;

Qy 4 LDP1QKLFVDKIREYKSKRQTSGGPVDASSSEYQOELERELFKLKQMGADMTPTPKF 63  
 Db 1440 LDKKQKAFDKVLSWKQKFEBSQALBNAQKRSRLGTFLFKLNAY-EETLDHLETPKR 1498

Qy 64 EDPKFE 69  
 Db 1499 ENKNLQ 1504

Search completed: April 4, 2005, 19:23:24  
 Job time : 120.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 19:11:13 ; Search time 26 Seconds  
(without alignments)  
281.249 Million cell updates/sec

Title: US-09-831-951a-1

Perfect score: 394  
Sequence: 1 NKEIDPIQKLFVDKIREYKS.....TFPTKPEDPKFEVLEKPKQA 76

Scoring table: BLAST62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	392	99.5	108	2	UT0563
2	346	87.8	108	1	UJB06
3	342	86.8	76	3	S00212
4	317	80.5	108	2	JC1167
5	29.5	20.2	1940	1	S04090
6	28.5	19.9	557	2	A61256
7	27.5	19.7	764	2	I51302
8	26.5	19.4	1940	1	A24922
9	25.5	19.2	1931	2	A59234
10	25.5	19.2	1934	2	I48153
11	25.5	19.2	1935	1	A37102
12	25.5	19.2	1938	1	S06005
13	25.5	19.2	1938	2	I49464
14	25.5	19.2	1939	1	A46762
15	25.5	19.2	1939	2	I48175
16	25.5	19.0	15	2	PD0444
17	23.5	18.7	1935	1	S06006
18	22.5	18.4	285	2	J00448
19	22.5	18.4	741	2	S39082
20	22.5	18.4	936	2	S39083
21	22.5	18.4	955	2	S24348
22	22.5	18.4	1940	2	A29320
23	21.5	18.1	1039	2	S18199
24	21.5	18.0	555	2	T13120
25	21.5	18.0	1176	2	S40899
26	20.5	17.9	824	2	AB3354
27	20.5	17.9	1938	1	JX0178
28	19.5	17.6	541	2	AE0464
29	19.5	17.6	929	2	T28927

30	69.5	17.6	1937	2	I38055	myosin heavy chain
31	69	17.5	436	2	B87374	Rea4 secretion sys
32	68.5	17.4	142	2	I50496	light meromyosin -
33	68	17.3	284	2	S17563	RNA-binding protei
34	68	17.3	342	2	A24263	myosin heavy chain
35	68	17.3	509	2	S45631	DNA primase chain
36	68	17.3	808	2	C72858	Acotf-66 protein -
37	67.5	17.3	1935	2	A59286	myosin heavy chain
38	67.5	17.1	302	2	S56751	single stranded D
39	67.5	17.1	353	1	S56750	single stranded D
40	67.5	17.1	2186	2	H89960	hypothetical prote
41	66.5	16.9	385	2	C24263	myosin heavy chain
42	65.5	16.6	793	1	SURFCA	endopeptidase Clp
43	65.5	16.6	1938	2	A59293	skeletal myosin he
44	65	16.5	143	2	A12057	hypothetical prote
45	65	16.5	217	2	G70407	hypothetical prote

## ALIGNMENTS

## RESULT 1

UT0563  
coupling factor 6 precursor, mitochondrial - human

N:Alternate names: ATP synthase coupling factor 6  
C:Species: Homo sapiens (man)

C:Date: 17-Apr-1993 #sequence revision 17-Apr-1993 #text\_change 09-Jul-2004

C:Accession: UT0563; Q01066; T14747

R:Javed, A.A.; Ogata, K.; Sanadi, D.R.  
Gene 97, 307-310, 1991

A:Title: Human mitochondrial ATP synthase: cloning cDNA for the nuclear-encoded precursors  
A:Reference number: UT0563; MUID:91153664; PMID:1825642

A:Accession: UT0563  
A:Molecule type: mRNA

A:Residues: 1-108 <JAV>  
A:Cross-references: UNIPROT:P18859; GB:M37104; NID:g179274; PIDN:AAA51807.1; PID:g179277

A:Cross-references: UNIPROT:P18859; GB:M37104; NID:g179274; PIDN:AAA51807.1; PID:g179277  
A:Experimental source: fetal muscle

R:Hiiguti, T.; Tsunumi, C.; Kawamura, Y.; Tsujita, H.; Osaka, F.; Yoshihara, Y.; Tani, I  
Biochem. Biophys. Res. Commun. 178, 793-799, 1991

A:Title: Molecular cloning of cDNA for the import precursor of human coupling factor 6  
A:Reference number: Q01066; MUID:91153516; PMID:1830479

A:Accession: Q01066  
A:Molecule type: mRNA

A:Residues: 1-67, 'H', 69-108 <HTG>  
A:Cross-references: GB:M73031; NID:g183785; PIDN:AAA58630.1; PID:g183786

A:Experimental source: kidney  
R:Blum, H.; Baerach, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, August 1999

A:Reference number: Z18179  
A:Accession: T14747

A:Status: preliminary  
A:Molecule type: mRNA

A:Residues: 1-108 <BLU>  
A:Cross-references: EMBL:AL10183

A:Experimental source: fetal kidney; clone DKFZ566A221  
C:Gene: GDB:ATP5J

A:Cross-references: GDB:127519  
A:Map position: 2pter-2qter

A>Note: DKFZ566A221.1  
C:Superfamily: coupling factor 6

C:Keywords: mitochondrial; oxidative phosphorylation  
F11-32/Domains: transist peptide (mitochondrion) #status predicted <TPP>

F13-108/Product: coupling factor 6 #status predicted <MAT>

Query Match 99.5%; Score 392; DB 2; Length 108;  
Best local similarity 98.7%; Pred. No. 4.9e-34;

Matches 75; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKEIDPIQKLFVDKIREYKSRQTSGGPVDASSSYQGLERELFKLQMGFNADMTPT 60  
DB 33 NKEIDPIQKLFVDKIREYKSRQTSGGPVDASSSYQGLERELFKLQMGFNADMTPT 92



A:Title: Nucleotide sequence of full length human embryonic myosin heavy chain cDNA.  
 A:Reference number: S04090; MUID:89263803; PMID:2726495  
 A:Accession: S04090  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-1940 <EHL>  
 A:Cross-references: UNIPROT:P11055; EMBL:X13988; NID:G34843; PIDN:CAA32167.1; PID:G34844  
 R:Eller, M.; Stedman, H.H.; Sylvester, J.E.; Fertels, S.H.; Wu, Q.L.; Raychowdhury, M.K.  
 FEBS Lett. 256, 21-28, 1989  
 A:Title: Human embryonic myosin heavy chain cDNA. Interspecies sequence conservation of  
 A:Reference number: S06146; MUID:9003298; PMID:2806546  
 A:Accession: S06146  
 A:Molecule type: mRNA  
 A:Residues: 774-1662, 'QT', 1665-1940 <EL2>  
 A:Cross-references: EMBL:X13100; NID:G31143; PIDN:CAA31492.1; PID:G31144  
 R:Karsch-Mizrachi, I.; Travis, M.; Blau, H.; Levinward, L.A.  
 Nucleic Acids Res. 17, 6167-6179, 1989  
 A:Title: Expression and DNA sequence analysis of a human embryonic skeletal muscle myosin  
 A:Reference number: S05442; MUID:89366648; PMID:2771643  
 A:Accession: S05442  
 A:Molecule type: DNA  
 A:Residues: 856-1390, 'KK', 1393-1940 <KAR>  
 A:Cross-references: EMBL:X15696; NID:G36504; PIDN:CAA3731.1; PID:G133513  
 R:Stedman, H.H.; Eller, M.; Jullian, E.H.; Fertels, S.H.; Sarkar, S.; Sylvester, J.E.; K  
 J. Biol. Chem. 265, 3568-3576, 1990  
 A:Title: The human embryonic myosin heavy chain. Complete primary structure reveals evol  
 A:Reference number: A35082; MUID:90154023; PMID:2303463  
 A:Contents: annotation; chromosomal assignment  
 R:Bober, E.  
 Submitted to the EMBL Data Library, January 1989  
 A:Reference number: S12458  
 A:Accession: S12458  
 A:Molecule type: mRNA  
 A:Residues: 856-1330, 'G', 1332-1390, 'KK', 1393-1607, 'RA', 1610-1940 <BOB>  
 A:Cross-references: EMBL:X51593; NID:G29463; PIDN:CAA35942.1; PID:G29464  
 A:Experimental source: clone gEMC-E  
 R:Bober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, H.H.  
 Eur. J. Biochem. 189, 55-65, 1990  
 A:Title: Identification of three developmentally controlled isoforms of human myosin hea  
 A:Reference number: S09331; MUID:90235862; PMID:1691980  
 A:Accession: S09331  
 A:Molecule type: mRNA  
 A:Residues: 856-901, 'X', 903-971, 'X', 973-1041, 'X', 1043-1111, 'X', 1113-1181, 'X', 1183-1251, '  
 1, 'X', 1673-1741, 'X', 1743-1811, 'X', 1813-1881, 'X', 1883-1940 <BOB>  
 A:Cross-references: EMBL:X51593  
 C:Genetics:  
 A:Gene: GDB:MYH3  
 A:Cross-references: GDB:119443; OMIM:160720  
 A:Map position: 17p13.1-17p13.1  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 C:Keywords: actin binding; ATP; coiled coil; hydrolyase; methylated amino acid; muscle co  
 F:89-767/Domain: myosin motor domain homology <MYOT>  
 F:119-186/Region: nucleotide-binding motif A (P-loop)  
 F:549-586/Region: actin binding #status predicted  
 F:656-678/Region: actin binding #status predicted  
 F:840-1940/Domain: coiled coil #status predicted <COI>  
 F:840-1280/Region: 52  
 F:1281-1940/Region: light meromyosin  
 F:130/Modified site: N6,N6-Crimethyllysine (lys) #status predicted  
 F:185/Binding site: ATP (lys) #status predicted  
 F:696,706/Active site: Cys #status predicted

Query Match 20.2%; Score 79.5; DB 1; Length 1940;  
 Best Local Similarity 33.3%; Pred. No. 6.1;  
 Matches 22; Conservative 13; Mismatches 30; Indels 1; Gaps 1;

4 LDPIQKLVNDKIRKYSKRTSGGPVDSSEYQOELRELFKTKOMFGNADMTPTPKF 63  
 Db 1443 LDKQKRNFDKVLAWKTKCESQAELEASLKESSLSLSTELFKLKNAYBEA-LDQLETVKR 1501

64 EDPKFE 69  
 Db 1502 ENKYLE 1507

RESULT 6  
 A61256  
 myosin heavy chain, skeletal muscle - rabbit (fragment)  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 12-May-1994 #sequence\_revision 12-May-1994 #text\_change 09-Jul-2004  
 C:Accession: A61256  
 R:Jackson, S.J.; Stewart, M.  
 J. Cell Sci. 99, 823-836, 1991  
 A:Title: Expression in Escherichia coli of fragments of the coiled-coil rod domain of r  
 A:Reference number: A61256; MUID:92121252; PMID:1770009  
 A:Accession: A61256  
 A:Molecule type: preliminary  
 A:Status: preliminary  
 A:Residues: 1-557 <ATK>  
 A:Cross-references: UNIPROT:Q7M3B1; GB:X59602  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 C:Keywords: ATP; skeletal muscle

Query Match 19.9%; Score 78.5; DB 2; Length 557;  
 Best Local Similarity 33.3%; Pred. No. 1.9;  
 Matches 22; Conservative 13; Mismatches 30; Indels 1; Gaps 1;

4 LDPIQKLVNDKIRKYSKRTSGGPVDSSEYQOELRELFKTKOMFGNADMTPTPKF 63  
 Db 60 LDKQKRNFDKVLAWKTKCESQAELEASLKESSLSLSTELFKLKNAYBEA-LDQLETVKR 118

64 EDPKFE 69  
 Db 119 ENKYLE 124

RESULT 7  
 I51302  
 myosin heavy chain - chicken (fragment)  
 C:Species: Gallus gallus (chicken)  
 C:Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 09-Jul-2004  
 C:Accession: I51302  
 R:Rutzy, K.E.; Rhee, J.T.; Bader, D.  
 Development 120, 871-883, 1994  
 A:Title: Expression of the atrial-specific myosin heavy chain AMHC1 and the establishe  
 A:Reference number: I51302; MUID:95324374; PMID:7600964  
 A:Accession: I51302  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-764 <YOT>  
 A:Cross-references: UNIPROT:Q91411; GB:S78540; NID:G1000404; PIDN:AAB34772.1; PID:G1000  
 C:Superfamily: myosin heavy chain; myosin motor domain homology

Query Match 19.7%; Score 77.5; DB 2; Length 764;  
 Best Local Similarity 33.3%; Pred. No. 3.4;  
 Matches 22; Conservative 12; Mismatches 31; Indels 1; Gaps 1;

4 LDPIQKLVNDKIRKYSKRTSGGPVDSSEYQOELRELFKTKOMFGNADMTPTPKF 63  
 Db 271 LDKQKRNFDKVLAWKTKCESQAELEASLKESSLSLSTELFKLKNAYBEA-LDQLETVKR 329

64 EDPKFE 69  
 Db 330 ENKYLE 335

RESULT 8  
 A24922  
 myosin heavy chain, skeletal muscle, embryonic - rat  
 N:Contains: myosin ATPase (BC 3.6.4.1)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
 C:Accession: A24922; A22538; B24263  
 R:Strehler, E.E.; Strehler-Pag, M.A.; Perriard, J.C.; Periaamy, M.; Nadal-Ginard, B.  
 J. Mol. Biol. 190, 291-317, 1986  
 A:Title: Complete nucleotide and encoded amino acid sequence of a mammalian myosin heavy



A>Title: Complete sequence and organization of the human cardiac beta-myosin heavy chain  
 A/Reference number: S12733; MUID:90301496; PMID:2362820  
 A/Accession: S12733  
 A/Molecule type: DNA  
 A/Residues: 1-106, 'E', 108-671, 'LYH', 675-857, 'A', 859-941, 'NV', 944-1123, 'A', 1125-1158, 'C',  
 A/Cross-references: EMBL:X52889; NID:929726; PIDD:CAA37068.1; PID:929727  
 R,Yamauchi,Takahara, K.; Sole, M.J.; Llew, J.; Ing, D.; Llew, C.C.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 3504-3508, 1989  
 A/Title: Characterization of human cardiac myosin heavy chain genes.  
 A/Reference number: A94224; MUID:89264452; PMID:2726733  
 A/Accession: A94224  
 A/Molecule type: DNA  
 A/Residues: 1-87, 'Q', 89-106, 'E', 108-177, 1325-1702, 'DR', 1705-1786, 1788-1803, 'E', 1804-1935  
 R,Yamauchi,Takahara, K.; Sole, M.J.; Llew, J.; Ing, D.; Llew, C.C.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 7416-7417, 1989  
 A/Reference number: A94226  
 A/Contents: annotation; erratum  
 R,Kunadyabhi, M.; Tsuchimochi, H.; Komuro, I.; Takaku, F.; Yazaki, Y.  
 J. Clin. Invest. 82, 524-531, 1988  
 A/Title: Molecular cloning and characterization of human cardiac alpha- and beta-form my  
 human actin.  
 A/Reference number: A92770; MUID:88299163; PMID:2965919  
 A/Accession: B28908  
 A/Molecule type: mRNA  
 A/Residues: 1412-1518, 'R', 1520-1574, 'NV', 1577-1935 <KOR>  
 A/Cross-references: GB:M21655  
 A/Note: the authors translated the codon AGC for residue 108 as Arg  
 R,Lichter, P.; Umada, P.K.; Levin, J.E.; Vosberg, H.P.  
 Eur. J. Biochem. 160, 419-426, 1986  
 A/Title: Partial characterization of the human beta-myosin heavy-chain gene which is exp  
 A/Reference number: A24997; MUID:87030293; PMID:3021460  
 A/Accession: A24997  
 A/Molecule type: DNA  
 A/Residues: 682-721, 975-1112, 1854-1935 <LIC>  
 A/Cross-references: GB:X04627  
 R,Saez, L.; Gianola, K.M.; McNally, E.M.; Feghali, R.; Eddy, R.; Shows, T.B.; Leinwand  
 Nucleic Acids Res. 15, 5443-5459, 1987  
 A/Title: Human cardiac myosin heavy chain genes and their linkage in the genome.  
 A/Reference number: A93669; MUID:87260010; PMID:3037493  
 A/Accession: A27858  
 A/Molecule type: DNA  
 A/Residues: 1854-1865, 'A', 1867-1935 <SAB>  
 A/Cross-references: GB:X05631; GB:Y00362; NID:934643; PIDD:CAA29119.1; PID:934644  
 R,Diederich, K.W.; Eiselle, I.; Ried, T.; Jaenicke, T.; Lichter, P.; Vosberg, H.P.  
 Hum. Genet. 81, 214-220, 1989  
 A/Title: Isolation and characterization of the complete human beta-myosin heavy chain ge  
 A/Reference number: 154254; MUID:89154425; PMID:2522082  
 A/Accession: 154254  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 653-720 <RES>  
 A/Cross-references: GB:M27636; NID:9179511; PIDD:AAA79019.1; PID:9601916  
 R,Bober, E.  
 submitted to the EMBL Data Library, January 1989  
 A/Reference number: S12458  
 A/Accession: S12458  
 A/Molecule type: mRNA  
 A/Residues: 785-1076, 'E', 1078-1123, 'A', 1125-1702, 'DE', 1705-1935 <BOB>  
 A/Cross-references: EMBL:X51591; NID:929467; PIDD:CAA35940.1; PID:929468  
 R,Bober, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goede, H.W.; Arnold, H.H.  
 Eur. J. Biochem. 189, 55-65, 1990  
 A/Title: Identification of three developmentally controlled isoforms of human myosin hea  
 A/Reference number: S09331; MUID:90235862; PMID:1691980  
 A/Accession: S09331  
 A/Molecule type: mRNA  
 A/Residues: 785-830, 'X', 832-900, 'X', 902-970, 'X', 972-1040, 'X', 1042-1076, 'E', 1078-1110, 'X',  
 '1602-1670, 'X', 1672-1702, 'DE', 1705-1740, 'X', 1742-1810, 'X', 1812-1935 <BOB>  
 A/Cross-references: EMBL:X51591  
 R,Jandreski, M.A.; Llew, C.C.  
 Hum. Genet. 76, 47-53, 1987  
 A/Title: Construction of a human ventricular cDNA library and characterization of a beta  
 A/Reference number: S02229; MUID:87192738; PMID:3032769  
 A/Accession: S02229

A/Molecule type: mRNA  
 A/Residues: 1393-1702, 'DR', 1705-1935 <JAN>  
 A/Cross-references: EMBL:X06976; NID:934860; PIDD:CAA30039.1; PID:9825694  
 R,Saez, L.; Leinwand, L.A.  
 Nucleic Acids Res. 14, 2951-2969, 1986  
 A/Title: Characterization of diverse forms of myosin heavy chain expressed in adult hum  
 A/Reference number: A93616; MUID:86176778; PMID:2421254  
 A/Accession: B23767  
 A/Molecule type: mRNA  
 A/Residues: 'LUGVEELASG', 1311-1312, 'G', 1314-1355, 'R', 1357-1358, 'GD', 1361-1438, 'LQ', 1441  
 A/Note: the first ten codons of the sequence figure show the reverse complementary stre  
 C,Genetics:  
 A/Gene: GDB:MYH7  
 A/Cross-references: GDB:120215; OMIM:160760  
 A/Map position: 14q12-14q12  
 A/Introns: 67/3; 115/3; 168/1; 177/2; 213/3; 244/3; 266/1; 299/1; 333/3; 380/1; 419/3;  
 24/3; 1390/2; 1451/3; 1507/1; 1548/3; 1651/3; 1719/3; 1761/3; 1853/3; 1885/3; 1930/3  
 C,Superfamily: myosin heavy chain; myosin motor domain homology  
 C,Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methylat  
 F,188-766/Domain: myosin motor domain homology <MMOT>  
 F,178-185/Region: nucleotide-binding motif 2 (P-loop)  
 F,548-585/Region: actin binding #status predicted  
 F,655-677/Region: actin binding #status predicted  
 F,839-1935/Domain: coiled coil #status predicted <COI>  
 F,839-1279/Region: S2  
 F,1280-1935/Region: light meromyosin  
 F,128/Modified site: N6,N6,N6-trimethyllysine (lys) #status predicted  
 F,184/Binding site: ATP (lys) #status predicted  
 F,695,705/Active site: Cys #status predicted  
 Query Match 19.2%; Score 75.5; DB 1; Length 1935;  
 Best Local Similarity 30.3%; Pred. No. 16;  
 Matches 20; Conservative 13; Mismatches 32; Indels 1; Gaps 1;  
 Db 4 LDPIQKLVFDKIREYKSKRQTSQGPVADSEYQELRELFKLMQMGNDMTPTPKF 63  
 1442 LDKQRNFDKILAEKQYKESQSELSQSEARSLSTELFKLNAV EESLEHLETFKR 1500  
 Qy 64 EDPKFE 69  
 Db 1501 ENKNLQ 1506  
 RESULT 12  
 S06005  
 myosin alpha heavy chain, cardiac muscle [similarity] - rat  
 N/Alternate names: alpha-myosin heavy chain  
 C/Species: myosin ATPase (EC 3.6.4.1)  
 C/Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
 C/Accession: S06005; S07535; A20971; A02988; I53305  
 R,McNally, E.M.; Gianola, K.M.; Leinwand, L.A.  
 Nucleic Acids Res. 17, 7527-7528, 1989  
 A/Title: Complete nucleotide sequence of full length cDNA for rat alpha cardiac myosin  
 A/Reference number: S06005; MUID:90016822; PMID:2798111  
 A/Accession: S06005  
 A/Status: translation not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-1938 <MCN>  
 A/Cross-references: UNIPROT:P02563; EMBL:X15938; NID:956654; PIDD:CAA34064.1; PID:95665  
 R,McNally, E.M.; Kraft, R.; Bravo-Zehnder, M.; Taylor, D.A.; Leinwand, L.A.  
 J. Mol. Biol. 210, 665-671, 1989  
 A/Title: Full-length rat alpha and beta cardiac myosin heavy chain sequences. Compariso  
 A/Reference number: S07535; MUID:90133919; PMID:2614840  
 A/Accession: S07535  
 A/Status: not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-1938 <MC2>  
 R,Mandavi, V.; Chambers, A.P.; Nadal-Ginard, B.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 2626-2630, 1984  
 A/Title: Cardiac alpha- and beta-myosin heavy chain genes are organized in tandem.  
 A/Reference number: A20971; MUID:84194059; PMID:6585819  
 A/Accession: A20971

A:Molecule type: protein  
 A:Residues: 112,'A',14-45,'A',47-50,'AP',53-61,'E',83-86,'Q',88-109,111-133,'H',135-16  
 R;Mahdavi, V.; Periasamy, M.; Nadal-Ginard, B.  
 Nature 297, 659-664, 1982  
 A:Title: Molecule characterization of two myosin heavy chain genes expressed in the adu  
 A:Reference number: A02988; MUID:82220036; PMID:7045682  
 A:Accession: A02988  
 A:Molecule type: mRNA  
 A:Residues: 1512-1574,'S',1576-1721,'N',1723-1851,'N',1853-1869,'N',1871-1933,'I',1935-1  
 A:Note: there are 10 or more myosin heavy chain genes in the rat, at least two of which  
 R;Mahdavi, V.; Lompre, A.M.; Chambers, A.P.; Nadal-Ginard, B.  
 Eur. Heart J. 5, 181-191, 1984  
 A:Title: Cardiac myosin heavy chain isozyemic transitions during development and under pa  
 A:Reference number: I53305; MUID:85179510; PMID:6241892  
 A:Accession: I53305  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1872-1933,'I',1935-1938 <RES>  
 A:Cross-references: GB:M32697; NID:g205596; PIDN:AAA41658.1; PID:g205597  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 C:Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methylate  
 F:87-767/Domain: myosin motor domain homology <MMOT>  
 F:177-184/Region: nucleotide-binding motif A (P-loop)  
 F:548-585/Region: actin binding #status predicted  
 F:666-678/Region: actin binding #status predicted  
 F:840-1938/Domain: coiled coil #status predicted <COI>  
 F:840-1280/Region: S2  
 F:1281-1938/Region: light meromyosin  
 F:128/Modified site: N6,N6,N6-trimethyllysine (lys) #status predicted  
 F:183/Binding site: ATP (lys) #status predicted  
 F:686,706/Active site: Cys #status predicted

Query Match 19.2%; Score 75.5; DB 1; Length 1938;  
 Best Local Similarity 30.3%; Pred. No. 16;  
 Matches 20; Conservative 13; Mismatches 32; Indels 1; Gaps 1;

QY 4 LDPDQKLPVDFKIRYKSKQTSQGPVDAASVQGLERELFKKQMGFNADMTTFPFK 63  
 DB 1443 LDKQRNPFDKILAEWKQKYESGSELSQKARSLSLELFKKNAY-EESLEHLETFK 1501

QY 64 EDPKFE 69  
 DB 1502 ENKMLQ 1507

# RESULT 13

149464

alpha cardiac myosin heavy chain - mouse  
 C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C:Accession: I49464; I49463; I49462; I49461; I49604

R;Quinn-Laquer, B.K.; Kennedy, J.E.; Wei, S.C.; Beisel, K.W.  
 Genomics 13, 176-188, 1992  
 A:Title: Characterization of the allelic differences in the mouse cardiac alpha-myosin h

A:Reference number: A38207; MUID:92250040; PMID:1577481

A:Accession: I49464  
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
 A:Residues: 1-1938 <RES>

A:Cross-references: UNIPROT:Q02566; GB:M76601; NID:g191623; PIDN:AAA37162.1; PID:g191624  
 A:Accession: I49463

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
 A:Residues: 1-193,'D',195-837,'S',839-955,'N',957-1938 <RES>

A:Cross-references: GB:M76600; NID:g191621; PIDN:AAA37161.1; PID:g191622  
 A:Accession: I49462

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA  
 A:Residues: 1-1938 <RES>

A:Cross-references: GB:M76599; NID:g191619; PIDN:AAA37160.1; PID:g191620  
 A:Accession: I49461

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-544,'A',546-1938 <RES>  
 A:Cross-references: GB:M76598; NID:g191617; PIDN:AAA37159.1; PID:g191618  
 R;Glick, J.; Subramaniam, A.; Neumann, J.; Robbins, J.  
 J. Biol. Chem. 266, 9180-9185, 1991  
 A:Title: Isolation and characterization of the mouse cardiac myosin heavy chain genes.  
 A:Reference number: I49604; MUID:91225025; PMID:2026617  
 A:Accession: I49604  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-67 <RES>  
 A:Cross-references: GB:M6204; NID:g192609; PIDN:AAA37424.1; PID:g192610  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 C:Keywords: ATP; cardiac muscle; heart; nucleotide binding; P-loop  
 F:88-768/Domain: myosin motor domain homology <MMOT>  
 F:178-185/Region: nucleotide-binding motif A (P-loop)

Query Match 19.2%; Score 75.5; DB 2; Length 1938;  
 Best Local Similarity 30.3%; Pred. No. 16;  
 Matches 20; Conservative 13; Mismatches 32; Indels 1; Gaps 1;

QY 4 LDPDQKLPVDFKIRYKSKQTSQGPVDAASVQGLERELFKKQMGFNADMTTFPFK 63  
 DB 1444 LDKQRNPFDKILAEWKQKYESGSELSQKARSLSLELFKKNAY-EESLEHLETFK 1502

QY 64 EDPKFE 69  
 DB 1503 ENKMLQ 1508

# RESULT 14

A46762  
 myosin alpha heavy chain, cardiac muscle - human

N:Contains: myosin ATPase (EC 3.6.4.1)  
 C:Species: Homo sapiens (man)

C>Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
 C:Accession: A46762; B46762; A49354; S18830; B32562; B33835; B27858; A28908

R;Matsuo, R.; Beisel, K.W.; Furutani, M.; Arai, S.; Takeao, A.  
 Am. J. Med. Genet. 41, 537-547, 1991

A:Title: Complete sequence of human cardiac alpha-myosin heavy chain gene and amino aci  
 A:Reference number: A46762; MUID:92133665; PMID:1776652

A:Accession: A46762

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-1939 <MAT>

A:Cross-references: UNIPROT:P13533; UNIPROT:Q90QV; DDBJ:D00943; NID:g219523; PIDN:BA01  
 A:Accession: B46762

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1461 <MA2>  
 R;Epp, T.A.; Dixon, I.M.C.; Wang, H.Y.; Sole, M.J.; Liew, C.C.

Genomics 18, 505-509, 1993  
 A:Title: Structural organization of the human cardiac alpha-myosin heavy chain gene (MY

A:Reference number: A49354; MUID:9410346; PMID:8307559

A:Accession: A49354

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-87,'Q',89-573,'Q',575-607,'A',609-743,'T',745-789,'M',791-1013,'V',1015-1  
 A:Cross-references: GB:Z20656; NID:g297023; PIDN:CAA79675.1; PID:g297024

A:Accession: I4939 <EBP>

A:Status: preliminary  
 A:Molecule type: mRNA

A:Residues: 1-32 <BRA>  
 A:Cross-references: EMBL:X56181; NID:g28318; PIDN:CAA39642.1; PID:g28319

R;Yamauchi-Takahara, K.; Sole, M.J.; Liew, J.; Ing, D.; Liew, C.C.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 3504-3508, 1989

A:Title: Characterization of the human cardiac myosin heavy chain genes.  
 A:Reference number: A94224; MUID:89264452; PMID:2726733

A:Accession: B32562





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 4, 2005, 18:55:50 ; Search time 94.5 Seconds  
(without alignments)  
266.678 Million cell updates/sec

Title: US-09-831-951A-1  
Perfect score: 394  
Sequence: 1 NKEIDPIQKLFVDKIREYKS.....TFPTFKEDPKFVLEKQQA 76

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 311592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
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7: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
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9: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	392	99.5	84	US-10-106-698-6594	Sequence 6594, Ap
2	392	99.5	108	US-10-131-410-119	Sequence 119, Ap
3	392	99.5	108	US-10-408-765A-1253	Sequence 1253, Ap
4	332	84.3	108	US-10-926-543-77	Sequence 77, Appl
5	112	28.4	56	US-09-864-761-33712	Sequence 33712, A
6	112	28.4	56	US-09-864-761-34125	Sequence 34125, A
7	79.5	20.2	1940	US-09-738-630-99	Sequence 99, Appl
8	79.5	20.2	1940	US-10-408-765A-1175	Sequence 1175, Ap
9	75.5	19.2	1137	US-10-336-472-16	Sequence 16, Appl
10	75.5	19.2	1185	US-10-350-797-3350	Sequence 3350, Ap
11	75.5	19.2	1859	US-10-336-472-20	Sequence 20, Appl
12	75.5	19.2	1935	US-10-336-472-22	Sequence 22, Appl
13	71	18.0	202	US-10-264-237-1904	Sequence 1904, Ap

14	71	18.0	567	15	US-10-108-260A-4464	Sequence 4464, Ap
15	70.5	17.9	892	14	US-10-205-219-102	Sequence 102, App
16	69.5	17.6	541	15	US-10-282-122A-77851	Sequence 77851, A
17	69.5	17.6	750	15	US-10-369-493-20521	Sequence 20521, A
18	69.5	17.6	1939	16	US-10-408-765A-2188	Sequence 2188, Ap
19	68.5	17.4	285	15	US-10-094-749-1655	Sequence 1655, Ap
20	68.5	17.4	332	15	US-10-108-260A-4506	Sequence 4506, Ap
21	67.5	17.1	744	15	US-10-369-493-7908	Sequence 7908, Ap
22	67.5	17.1	1941	16	US-10-437-963-171741	Sequence 171741, A
23	67.5	17.1	1983	15	US-10-282-122A-43976	Sequence 43976, A
24	67.5	17.1	2076	9	US-09-815-242-5815	Sequence 5815, Ap
25	67.5	17.1	2186	9	US-09-815-242-12913	Sequence 12913, A
26	67.5	17.0	2186	9	US-10-470-048B-336	Sequence 336, App
27	67	16.9	479	15	US-10-282-122A-72411	Sequence 72411, A
28	66.5	16.9	1184	15	US-10-282-122A-53254	Sequence 53254, A
29	66	16.8	711	9	US-09-748-875-3	Sequence 3, Appli
30	66	16.8	711	10	US-09-298-523B-3	Sequence 3, Appli
31	66	16.8	6641	15	US-10-282-122A-70580	Sequence 70580, A
32	66	16.8	10203	16	US-10-661-809-23	Sequence 23, Appl
33	65.5	16.6	507	15	US-10-282-122A-60276	Sequence 60276, A
34	65.5	16.6	740	15	US-10-369-493-21798	Sequence 21798, A
35	65.5	16.6	822	15	US-10-369-493-11834	Sequence 11834, A
36	65.5	16.6	2189	14	US-10-172-502-2	Sequence 2, Appli
37	65	16.5	651	15	US-10-614-076-52	Sequence 52, Appli
38	65	16.5	652	14	US-10-232-665-2	Sequence 2, Appli
39	65	16.5	652	14	US-10-232-665-4	Sequence 4, Appli
40	65	16.5	652	14	US-10-232-665-6	Sequence 6, Appli
41	65	16.5	652	15	US-10-614-076-4	Sequence 4, Appli
42	65	16.5	652	15	US-10-614-076-6	Sequence 6, Appli
43	65	16.5	652	15	US-10-614-076-8	Sequence 8, Appli
44	65	16.5	652	15	US-10-614-076-10	Sequence 10, Appl
45	65	16.5	652	15	US-10-614-076-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1  
US-10-106-698-6594  
; Sequence 6594, Application US/10106698  
; Publication No. US20030109690A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OR INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptic  
; FILE REFERENCE: P4005P1  
; CURRENT APPLICATION NUMBER: US/10/106,698  
; PRIOR FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: PCT/US00/26524  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/157,137  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: US 60/163,280  
; PRIOR FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 8564  
; SOFTWARE: PatentIn Ver. 3.0  
; SEQ ID NO 6594  
; LENGTH: 84  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-106-698-6594  
Query Match 99.5%; Score 392; DB 14; Length 84;  
Best Local Similarity 98.7%; Pred. No. 4.8e-38;  
Matches 75; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 NKEIDPIQKLFVDKIREYKSKRTSGGPVNASSEYQOELRELFKLMKMGNAADMTPEPT 60  
Db 9 NKEIDPIQKLFVDKIREYKSKRTSGGPVNASSEYQOELRELFKLMKMGNAADMTPEPT 68  
OY 61 FKPEDPKFVLEKQQA 76  
Db 69 FKPEDPKFVLEKQQA 84



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1  PRIOR FILING DATE: 2001-01-30
2  PRIOR APPLICATION NUMBER: PCT/US01/00665
3  PRIOR FILING DATE: 2001-01-30
4  PRIOR APPLICATION NUMBER: PCT/US01/00668
5  PRIOR FILING DATE: 2001-01-30
6  PRIOR APPLICATION NUMBER: PCT/US01/00663
7  PRIOR FILING DATE: 2001-01-30
8  PRIOR APPLICATION NUMBER: PCT/US01/00662
9  PRIOR FILING DATE: 2001-01-30
10 PRIOR APPLICATION NUMBER: PCT/US01/00661
11 PRIOR FILING DATE: 2001-01-30
12 PRIOR APPLICATION NUMBER: PCT/US01/00670
13 PRIOR FILING DATE: 2001-01-30
14 PRIOR APPLICATION NUMBER: US 60/234,687
15 PRIOR FILING DATE: 2000-09-21
16 PRIOR APPLICATION NUMBER: US 09/608,408
17 PRIOR FILING DATE: 2000-06-30
18 PRIOR APPLICATION NUMBER: US 09/774,203
19 PRIOR FILING DATE: 2001-01-29
20 NUMBER OF SEQ ID NOS: 49117
21 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
22 SEQ ID NO 33712
23 LENGTH: 56
24 TYPE: PRT
25 ORGANISM: Homo sapiens
26 FEATURE:
27 OTHER INFORMATION: MAP TO AP000087.1
28 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3
29 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3
30 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
31 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.2
32 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
33 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
34 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.6
35 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4.9
36 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5
37 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
38 OTHER INFORMATION: SWISSPROT HIT: P18859, EVALU 5.00e-24
39 OTHER INFORMATION: EST_HUMAN HIT: AA128761.1, EVALU 5.00e-24
40 US-09-864-761-33712
41
42 Query Match 28.4% Score 112; DB 9; Length 56;
43 Best Local Similarity 100.0%; Pred. No. 1,4e-05;
44 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
45
46 Oy 1 NKELDPIQKLFVDKIREYKSKR 22
47 |||||
48 Db 35 NKELDPIQKLFVDKIREYKSKR 56
49
50 RESULT 6
51 US-09-864-761-34125
52 Sequence 34125, Application US/09864761
53 Patent No. US20020048763A1
54 GENERAL INFORMATION:
55 APPLICANT: Penn, Sharon G.
56 APPLICANT: Rank, David R.
57 APPLICANT: Hanzel, David K.
58 APPLICANT: Chen, Wensheng
59 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
60 FILE REFERENCE: Aecm1ca-X-1
61 CURRENT APPLICATION NUMBER: US/09/864,761
62 CURRENT FILING DATE: 2001-05-23
63 PRIOR APPLICATION NUMBER: US 60/180,312
64 PRIOR FILING DATE: 2000-02-04
65 PRIOR APPLICATION NUMBER: US 60/207,456
66 PRIOR FILING DATE: 2000-05-26
67 PRIOR APPLICATION NUMBER: US 09/632,366
68 PRIOR FILING DATE: 2000-06-03
69 PRIOR APPLICATION NUMBER: GB 24263.6
70 PRIOR FILING DATE: 2000-10-04
71 PRIOR APPLICATION NUMBER: US 60/236,359

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PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00662
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00661
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00670
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILING DATE: 2000-09-21
PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 34125
LENGTH: 56
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AP000139.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN HB1.100, SIGNAL = 5.2
OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.5
OTHER INFORMATION: EST HUMAN HIT: AAL28761.1, EVALUATE 5.00e-24
OTHER INFORMATION: SWISSPROT HIT: P18859, EVALUATE 5.00e-24
US-09-864-761-34125
Query Match 28.4%; Score 112; DB 9; Length 56;
Best Local Similarity 100.0%; Pred. No. 1,4e-05;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 NKELDPIQCLFVDKIREYKSKR 22
|||||
Db 35 NKELDPIQCLFVDKIREYKSKR 56
|||||
RESULT 7
US-09-738-630-99
Sequence 99, Application US/09738630
Publication No. US2003016213A1
GENERAL INFORMATION:
APPLICANT: Greenspan, Ralph J.
TITLE OF INVENTION: Methods For Identifying Compounds That
TITLE OF INVENTION: Modulate Disorders Related To Nitric Oxide/ cGMP-Dependent
FILE REFERENCE: P-NI 3906
CURRENT FILING DATE: US/09/738,630
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 4.0

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SEQ ID NO 99  
LENGTH: 1940  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-738-630-99

Query Match 20.2%; Score 79.5; DB 10; Length 1940;  
Best Local Similarity 33.3%; Pred. No. 7;  
Matches 22; Conservative 13; Mismatches 30; Indels 1; Gaps 1;

QY 4 LDPQLKLVDFKIREYKSRQTSQGGPVDAASSEYQQLERELFKLQMGFNADMTPTPTPKF 63  
DB 1443 LDKQRNDFKVLAEWKTCESQAELESLKESRSLSTELFKLKNAYEEA-LDQLETVKR 1501

QY 64 EDPKFE 69  
DB 1502 ENKNLE 1507

RESULT 8  
US-10-408-765A-1175  
Sequence 1175, Application US/10408765A  
Publication No. US20040101874A1

GENERAL INFORMATION:  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Zhang, Bing  
APPLICANT: Fahy, Eoin D.  
APPLICANT: Gibson, Bradford W.  
APPLICANT: Taylor, Steven W.  
APPLICANT: Glenn, Gary W.  
APPLICANT: Warnock, Dale E.  
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
FILE REFERENCE: 660088.465  
CURRENT APPLICATION NUMBER: US/10/408,765A  
CURRENT FILING DATE: 2003-04-04  
NUMBER OF SEQ ID NOS: 3077  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1175  
LENGTH: 1940  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-408-765A-1175

Query Match 20.2%; Score 79.5; DB 16; Length 1940;  
Best Local Similarity 33.3%; Pred. No. 7;  
Matches 22; Conservative 13; Mismatches 30; Indels 1; Gaps 1;

QY 4 LDPQLKLVDFKIREYKSRQTSQGGPVDAASSEYQQLERELFKLQMGFNADMTPTPTPKF 63  
DB 1443 LDKQRNDFKVLAEWKTCESQAELESLKESRSLSTELFKLKNAYEEA-LDQLETVKR 1501

QY 64 EDPKFE 69  
DB 1502 ENKNLE 1507

RESULT 9  
US-10-336-472-16  
Sequence 16, Application US/10336472  
Publication No. US20040043929A1

GENERAL INFORMATION:  
APPLICANT: Anderson, David W.  
APPLICANT: Ballinger, Robert A.  
APPLICANT: Baumgartner, Jason C.  
APPLICANT: Burgess, Catherine E.  
APPLICANT: Casman, Seacie J.  
APPLICANT: Chant, John S.  
APPLICANT: Berghs, Constance  
APPLICANT: Gangoli, Beha A.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Ellerman, Karen  
APPLICANT: Furtak, Katarzyna

APPLICANT: Gerlach, Valerie  
APPLICANT: Gilbert, Jennifer A.  
APPLICANT: Gunther, Erik  
APPLICANT: Gorman, Linda  
APPLICANT: Guo, Xiaojia Saaba  
APPLICANT: Ji, Weizhen  
APPLICANT: Li, Xiaohong  
APPLICANT: Miller, Charles E.  
APPLICANT: Padigar, Murailidhara  
APPLICANT: Patturajan, Meera  
APPLICANT: Rastelli, Luca  
APPLICANT: MacDougall, John R.  
APPLICANT: Mishra, Vishnu  
APPLICANT: Pena, Carol E.A.  
APPLICANT: Spaderma, Steven K.  
APPLICANT: Shinkets, Richard A.  
APPLICANT: Smithson, Glenda  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Stone, David J.  
APPLICANT: Shenoy, Suresh G.  
APPLICANT: Ort, Tatiana  
APPLICANT: Taupier Jr, Raymond J.  
APPLICANT: Tchernyev, Velizar T.  
APPLICANT: Vermet, Corine A.M.  
APPLICANT: Wolenc, Adam R.  
APPLICANT: Zerhusen, Bryan D.  
APPLICANT: Zhong, Wei  
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: 21402-533C  
CURRENT APPLICATION NUMBER: US/10/336,472  
CURRENT FILING DATE: 2003-01-03  
PRIOR APPLICATION NUMBER: 09/746,491  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: 10/005,041  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 10/023,681  
PRIOR FILING DATE: 2001-12-18  
PRIOR APPLICATION NUMBER: 10/024,212  
PRIOR FILING DATE: 2001-12-18  
PRIOR APPLICATION NUMBER: 10/055,569  
PRIOR FILING DATE: 2001-10-26  
PRIOR APPLICATION NUMBER: 10/080,334  
PRIOR FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 10/092,900  
PRIOR FILING DATE: 2002-03-07  
PRIOR APPLICATION NUMBER: 10/136,826  
PRIOR FILING DATE: 2002-05-01  
PRIOR APPLICATION NUMBER: 10/236,417  
PRIOR FILING DATE: 2002-09-06  
PRIOR APPLICATION NUMBER: 60/345,092  
PRIOR FILING DATE: 2002-01-04  
Remaining Prior Application data removed - See file wrapper or PAM.  
NUMBER OF SEQ ID NOS: 230  
SOFTWARE: CuraSeqList version 0.1  
SEQ ID NO 16  
LENGTH: 1137  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-336-472-16

Query Match 19.2%; Score 75.5; DB 15; Length 1137;  
Best Local Similarity 30.3%; Pred. No. 11;  
Matches 20; Conservative 13; Mismatches 32; Indels 1; Gaps 1;

QY 4 LDPQLKLVDFKIREYKSRQTSQGGPVDAASSEYQQLERELFKLQMGFNADMTPTPTPKF 63  
DB 644 LDKQRNDFKVLAEWKTCESQAELESLKESRSLSTELFKLKNAY-ESLEHLETFKR 702

QY 64 EDPKFE 69  
DB 703 ENKNLE 708

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RESULT 10
US-10-330-797-3350
; Sequence 3350, Application US/10320797
; Publication No. US20040014955A1
; GENERAL INFORMATION:
; APPLICANT: Eroshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: Patent version 3.1
; SEQ ID NO 3350
; LENGTH: 1185
; TYPE: PRT
; ORGANISM: Cryptococcus neoformans
US-10-320-797-3350

Query Match          19.2%; Score 75.5; DB 15; Length 1185;
Best Local Similarity 39.1%; Pred. No. 11;
Matches 18; Conservative 9; Mismatches 18; Indels 1; Gaps 1;

Qy      2 KELDPIQLFVDKIRKYSKRQTSGGPVDASSSEYQOELRELFKIK 47
Db      278 KECHGMEK-ELBEIRKKKEQAKGKIQGLTEAVNNIERELVYKIK 322

RESULT 11
US-10-336-472-20
; Sequence 20, Application US/10336472
; Publication No. US20040043929A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.
; APPLICANT: Ballinger, Robert A.
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Chant, John S.
; APPLICANT: Berghs, Constance
; APPLICANT: Gangolli, Esna A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gilbert, Jennifer A.
; APPLICANT: Gunther, Erik
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigar, Muralihara
; APPLICANT: Paturajan, Meera
; APPLICANT: Raetelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Mishra, Vishnu
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Shinkens, Richard A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Stone, David J.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Ort, Tatiana
; APPLICANT: Taupier Jr, Raymond J.
```

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; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Verneet, Corine A.M.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Zehrusen, Bryan D.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-533C
; CURRENT APPLICATION NUMBER: US/10/336,472
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: 09/746,491
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 10/005,041
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 10/023,681
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 10/024,212
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 10/055,569
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 10/080,334
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/092,900
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 10/136,826
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 10/236,417
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 60/345,092
; PRIOR FILING DATE: 2002-01-04
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 20
; LENGTH: 1859
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-336-472-20

Query Match          19.2%; Score 75.5; DB 15; Length 1859;
Best Local Similarity 30.3%; Pred. No. 19;
Matches 20; Conservative 13; Mismatches 32; Indels 1; Gaps 1;

Qy      4 LDPQLKLFVDKIRKYSKRQTSGGPVDASSSEYQOELRELFKIKQMGNADMTPTPKF 63
Db      1442 LDKQKRNFDKILAWKQKREBSQSELSQKQARSSTELFKLNAY-EESLEHLPTPKR 1500

Qy      64 EDPKFE 69
Db      1501 ENKMLQ 1506

RESULT 12
US-10-336-472-22
; Sequence 22, Application US/10336472
; Publication No. US20040043929A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W.
; APPLICANT: Ballinger, Robert A.
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Chant, John S.
; APPLICANT: Berghs, Constance
; APPLICANT: Gangolli, Esna A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gilbert, Jennifer A.
; APPLICANT: Gunther, Erik
; APPLICANT: Gorman, Linda
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Ji, Weizhen
```

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APPPLICANT: Li, Xiaohong
APPPLICANT: Miller, Charles E.
APPPLICANT: Miller, Isabelle
APPPLICANT: Padigaru, Muralidhara
APPPLICANT: Patnirajan, Meera
APPPLICANT: Rastelli, Luca
APPPLICANT: MacDougall, John R.
APPPLICANT: Mishra, Vishnu
APPPLICANT: Pena, Carol E.A.
APPPLICANT: Spaderna, Steven K.
APPPLICANT: Shinkets, Richard A.
APPPLICANT: Smithson, Glenda
APPPLICANT: Spytek, Kimberly A.
APPPLICANT: Stone, David J.
APPPLICANT: Shenoy, Suresh G.
APPPLICANT: Ort, Tatiana
APPPLICANT: Taupier Jr, Raymond J.
APPPLICANT: Tchiernev, Veilizar T.
APPPLICANT: Vernet, Corine A.M.
APPPLICANT: Wolenc, Adam R.
APPPLICANT: Zernusen, Bryan D.
APPPLICANT: Zhong, Mei
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-533C
CURRENT APPLICATION NUMBER: US/10/336,472
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: 09/746,491
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 10/005,041
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 10/023,681
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 10/024,212
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 10/055,569
PRIOR FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: 10/080,334
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 10/092,900
PRIOR FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 10/136,826
PRIOR FILING DATE: 2002-05-01
PRIOR APPLICATION NUMBER: 10/236,417
PRIOR FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 60/345,092
PRIOR FILING DATE: 2002-01-04
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 230
SOFTWARE: Curnaseq1st version 0.1
SEQ ID NO: 22
LENGTH: 1935
TYPE: PRT
ORGANISM: Homo sapiens
US-10-336-472-22

Query Match 19.2%; Score 75.5; DB 15; Length 1935;
Best Local Similarity 30.3%; Pred. No. 20;
Matches 20; Conservative 13; Mismatches 32; Indels 1; Gaps 1;

QY 4 LDPIDKLEVDKIREYKSRKQTSGGVDASSSEYQCLERELFKLXKMPGNADMTPEPPKF 63
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1442 LDKQGRNPDKILAEKKQYEEQSLSSESSQKEARSLSTELFKKNAY-EESLHEHLEPKR 15000
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 EDPKFE 69
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1501 ENKNIQ 1506
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
US-10-264-237-1904
; Sequence 1904, Application US/10264237
; Publication No. US20040009491A1

```

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; GENERAL INFORMATION:  
; APPLICANT: Birste et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P4131P1  
; CURRENT APPLICATION NUMBER: US/10/264,237  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/16450  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/205,515  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 2876  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 1904  
; LENGTH: 202  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC_FEATURE  
; LOCATION: (2)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: MISC_FEATURE  
; LOCATION: (3)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: MISC_FEATURE  
; LOCATION: (4)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: MISC_FEATURE  
; LOCATION: (8)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: MISC_FEATURE  
; LOCATION: (196)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
US-10-264-237-1904
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Query Match 18.0%; Score 71; DB 15; Length 202;  
Best Local Similarity 36.2%; Pred. No. 4.1;  
Matches 21; Conservative 7; Mismatches 22; Indels 8; Gaps 2;

Db 13 DKIREYKS-----KRQTSGGPVDAASEYYOELERELFKLKOMF--GNADMTFPPTKX 62  
          |      ||      |      |      |      |      |      |      |      |  
62 EKHCPEQALDHFKTKTKMGKGDFSPRYOOELEEEIKELYENPCKNNGSKNVFSTR 119

RESULT 14  
US-10-108-260A-4464  
; Sequence 4464, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: NO. US20040005560A1el full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4464  
; LENGTH: 567  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-108-260A-4464

Query Match 18.0%; Score 71; DB 15; Length 567;  
Best Local Similarity 36.2%; Pred. No. 15;  
Matches 21; Conservative 7; Mismatches 22; Indels 8; Gaps 2;

Db 13 DKIREYKS-----KRQTSGGPVDAASEYYOELERELFKLKOMF--GNADMTFPPTKX 62  
          |      ||      |      |      |      |      |      |      |      |  
411 EKHCPEQALDHFKTKTKMGKGKDPSFRYOOLEEIEEKLEYENPCKNNGSKNVFSTR 468



## RESULT 15

US-10-205-219-102  
; Sequence 102, Application US/10205219  
; Publication No. US20030138803A1  
; GENERAL INFORMATION:  
; APPLICANT: Warner-Lambert Company  
; APPLICANT: Lee, Kevin  
; APPLICANT: Dixon, Alister  
; APPLICANT: Brookbank, Robert  
; APPLICANT: Pincock, Robert  
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain  
; FILE REFERENCE: WL-A-018200  
; CURRENT APPLICATION NUMBER: US/10/205,219  
; CURRENT FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: GB 0118354.0  
; PRIOR FILING DATE: 2001-07-27  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 102  
; LENGTH: 892  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Myosin heavy chain  
US-10-205-219-102

Query Match 17.9%; Score 70.5; DB 14; Length 892;

Best Local Similarity 27.3%; Pred. No. 30; Mismatches 32; Indels 1; Gaps 1;  
Matches 18; Conservative 15;

QY 4 LDPIQLFVDDKIREYKSKRQTSQGVDAASSEYQQLERELPFLKQMGADWNTPTPKF 63  
DB 399 LDKQGRNEDKILAEWKQKYETHTALEASQKESRSLSTLFLKINAY-BESLDQLETLKR 457  
QY 64 EDPKFE 69  
DB 458 ENKNLQ 463

Search completed: April 4, 2005, 19:15:02  
Job time : 95.5 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 4, 2005, 18:46:29 ; Search time 30 Seconds  
(without alignments)  
189.111 Million cell updates/sec

Title: US-09-831-951A-1  
Perfect score: 394  
Sequence: 1 NKEIDPIQKLFVDKIREYKS.....TFPTKFEDEPKFEVLEKRPQA 76

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfilest.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	392	99.5	108	4	US-09-513-999C-8086
2	392	99.5	108	4	US-09-949-016-11049
3	387	98.2	108	2	US-08-828-239-3
4	387	98.2	108	3	US-09-205-679-3
5	383	97.2	106	4	US-09-513-999C-5967
6	346	87.8	108	2	US-08-828-239-4
7	346	87.8	108	3	US-09-205-679-4
8	325	82.5	114	2	US-08-828-239-1
9	325	82.5	114	3	US-09-205-679-1
10	317	80.5	108	2	US-08-828-239-5
11	317	80.5	108	3	US-09-205-679-5
12	185	47.0	69	4	US-09-513-999C-5968
13	79.5	20.2	1940	4	US-09-538-092-901
14	79.5	20.2	1963	4	US-09-949-016-8888
15	75.5	19.2	1886	3	US-08-938-105-3
16	75.5	19.2	1935	4	US-09-538-092-916
17	75.5	19.2	1939	3	US-09-310-187A-1
18	75.5	19.2	1939	4	US-09-538-092-917
19	75.5	19.2	1944	4	US-09-949-016-10929
20	69.5	17.6	1937	4	US-09-538-092-918
21	69.5	17.6	1939	4	US-09-538-092-915
22	69.5	17.6	1939	4	US-09-949-016-6925
23	69.5	17.6	1939	4	US-09-949-016-11104
24	69.5	17.6	1942	4	US-09-949-016-8135
25	68.5	17.4	215	4	US-09-949-016-7173
26	68.5	17.4	217	1	US-08-390-858B-9
27	68	17.3	284	1	US-08-390-858B-36

28	67.5	17.1	134	4	US-09-248-796A-17771	Sequence 17771, A
29	67.5	17.1	555	3	US-09-813-872-4	Sequence 4, Appl1
30	66	16.8	706	4	US-09-538-092-1266	Sequence 1266, Ap
31	66	16.8	1095	4	US-09-710-279-3154	Sequence 3154, Ap
32	66	16.8	10182	3	US-09-134-001C-3159	Sequence 3159, Ap
33	65.5	16.6	206	4	US-09-949-016-6411	Sequence 6411, Ap
34	65.5	16.6	520	4	US-09-489-039A-11079	Sequence 11079, A
35	65	16.5	551	3	US-08-996-441B-52	Sequence 52, Appl1
36	65	16.5	651	3	US-08-993-170A-52	Sequence 52, Appl1
37	65	16.5	651	3	US-08-993-170A-52	Sequence 52, Appl1
38	65	16.5	651	3	US-08-993-170A-52	Sequence 52, Appl1
39	65	16.5	651	4	US-09-427-770-52	Sequence 52, Appl1
40	65	16.5	651	4	US-09-427-769-52	Sequence 52, Appl1
41	65	16.5	652	3	US-08-996-441B-6	Sequence 4, Appl1
42	65	16.5	652	3	US-08-996-441B-6	Sequence 6, Appl1
43	65	16.5	652	3	US-08-996-441B-8	Sequence 8, Appl1
44	65	16.5	652	3	US-08-996-441B-10	Sequence 10, Appl1
45	65	16.5	652	3	US-08-996-441B-12	Sequence 12, Appl1

## ALIGNMENTS

```
RESULT 1
US-09-513-999C-8086
Sequence 8086, Application US/0951399C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59. US2. REG
CURRENT APPLICATION NUMBER: US/09/513.999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 8086
LENGTH: 108
TYPE: PRT
ORGANISM: Homo sapiens
US-09-513-999C-8086

Query Match          99.5%; Score 392; DB 4; Length 108;
Best Local Similarity 98.7%; Pred. No. 1.4e-39;
Matches 75; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKEIDPIQKLFVDKIREYKSGPVDASSYQDELRELFKTKOMFGNADMTFFPT 60
    |||
DB 33 NKEIDPIQKLFVDKIREYKSKRQTSKQTSVAVSSYQDELRELFKTKOMFGNADMTFFPT 92
    |||
QY 61 FKFEDEPKFEVLEKRPQA 76
    |||
DB 93 FKFEDEPKFEVLEKRPQA 108

RESULT 2
US-09-949-016-11049
Sequence 11049, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949.016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11049  
LENGTH: 108  
TYPE: PRF  
ORGANISM: Human  
US-09-949-016-11049

Query Match 99.5%; Score 392; DB 4; Length 108;  
Best Local Similarity 98.7%; Pred. No. 1,4e-39;  
Matches 75; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKELDPIQKLFVNDKIREYKSKRQTSQGPVDASSEYQOELERELFKLKOMFGNADMTTFPT 60  
DB 33 NKELDPIQKLFVNDKIREYKSKRQTSQGPVDASSEYQOELERELFKLKOMFGNADMTTFPT 92

QY 61 FKFEDEPKFEVLEKPOA 76  
DB 93 FKFEDEPKFEVLEKPOA 108

RESULT 3  
US-08-828-239-3  
Sequence 3, Application US/08828239  
Patent No. 5849527

GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.

APPLICANT: Shah, Puri  
TITLE OF INVENTION: NOVEL ATP SYNTHASE COUPLING FACTOR 6  
NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/828,239  
FILING DATE: Herewith

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0260 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166

TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 183786  
US-08-828-239-3

Query Match 98.2%; Score 387; DB 2; Length 108;  
Best Local Similarity 97.4%; Pred. No. 5,7e-39;

Matches 74; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NKELDPIQKLFVNDKIREYKSKRQTSQGPVDASSEYQOELERELFKLKOMFGNADMTTFPT 60  
DB 33 NKELDPIQKLFVNDKIREYKSKRQTSQGPVDASSEYQOELERELFKLKOMFGNADMTTFPT 92

QY 61 FKFEDEPKFEVLEKPOA 76  
DB 93 FKFEDEPKFEVLEKPOA 108

RESULT 4  
US-09-205-679-3  
Sequence 3, Application US/09205679  
Patent No. 6048718

GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.

APPLICANT: Shah, Puri  
TITLE OF INVENTION: NOVEL ATP SYNTHASE COUPLING FACTOR 6  
NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/205,679  
FILING DATE: Herewith

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/828,239  
FILING DATE: 03/31/1997

ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0260 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166

TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 183786  
US-09-205-679-3

Query Match 98.2%; Score 387; DB 3; Length 108;  
Best Local Similarity 97.4%; Pred. No. 5,7e-39;  
Matches 74; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NKELDPIQKLFVNDKIREYKSKRQTSQGPVDASSEYQOELERELFKLKOMFGNADMTTFPT 60  
DB 33 NKELDPIQKLFVNDKIREYKSKRQTSQGPVDASSEYQOELERELFKLKOMFGNADMTTFPT 92

QY 61 FKFEDEPKFEVLEKPOA 76  
DB 93 FKFEDEPKFEVLEKPOA 108

RESULT 5  
US-09-513-999C-5967

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; Sequence 5967, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5967
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-513-999C-5967

Query Match          97.2%; Score 383; DB 4; Length 106;
Best Local Similarity 98.6%; Pred. No. 1.7e-38;
Matches 73; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 NKELDPIQKLFVDKIREYKSKRQTSGGPVDASSEYQQLERELFKLKMPGNADMTPT 60
DB 33 NKELDPIQKLFVDKIREYKSKRQTSGGPVDASSEYQQLERELFKLKMPGNADMTPT 92

QY 61 FKPEDPKFEVLEKRP 74
DB 93 FKPEDPKFEVLEKRP 106

RESULT 6
US-08-828-239-4
; Sequence 4, Application US/08828239
; Patent No. 5849527
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL ATP SYNTHASE COUPLING FACTOR 6
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/828,239
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0260 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 625323
; US-08-828-239-4

Query Match          87.8%; Score 346; DB 2; Length 108;
Best Local Similarity 82.9%; Pred. No. 4.7e-34;
Matches 63; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 NKELDPIQKLFVDKIREYKSKRQTSGGPVDASSEYQQLERELFKLKMPGNADMTPT 60
DB 33 NKELDPIQKLFVDKIREYKSKRQTSGGPVDASSEYQQLERELFKLKMPGNADMTPT 92

QY 61 FKPEDPKFEVLEKRP 76
DB 93 FKPEDPKFEVLEKRP 108

RESULT 7
US-09-205-679-4
; Sequence 4, Application US/09205679
; Patent No. 6048718
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NOVEL ATP SYNTHASE COUPLING FACTOR 6
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/205,679
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/828,239
; FILING DATE: 03/31/1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0260 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 625323
; US-09-205-679-4

Query Match          87.8%; Score 346; DB 3; Length 108;
Best Local Similarity 82.9%; Pred. No. 4.7e-34;
Matches 63; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 NKELDPIQKLFVDKIREYKSKRQTSGGPVDASSEYQQLERELFKLKMPGNADMTPT 60
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Db 33 NKEIDPVOKLFDVCKIREYRTKQTSQGVADGPEYQOCDLDRLEFKLKQMGKADMTFFN 92  
QY 61 FKFEDEPKFEVLEKPOA 76  
Db 93 FTFEDEPKFEVLEKPOS 108

## RESULT 8

US-08-828-239-1  
; Sequence 1, Application US/08828239  
; Patent No. 5849527  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: NOVEL ATP SYNTHASE COUPLING FACTOR 6  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/828,239  
; FILING DATE: Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0260 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 114 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: Consensus  
; CLONE: 2496341  
US-08-828-239-1

Query Match 82.5%; Score 325; DB 2; Length 114;  
Best Local Similarity 98.4%; Pred. No. 1.6e-31;  
Matches 62; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 KIREYKSKRQTSQGVADASSYQOELERELFKLKQMGADNMTFFTFKFEDEPKFEVLEK 73  
Db 52 KIREYKSKRQTSQGVADASSYQOELERELFKLKQMGADNMTFFTFKFEDEPKFEVLEK 111  
QY 74 POA 76  
Db 112 POA 114

RESULT 9  
US-09-205-679-1  
; Sequence 1, Application US/09205679  
; Patent No. 6048718  
; GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: NOVEL ATP SYNTHASE COUPLING FACTOR 6  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/205,679  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/828,239  
FILING DATE: 03/31/1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0260 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 114 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: Consensus  
CLONE: 2496341  
US-09-205-679-1

Query Match 82.5%; Score 325; DB 3; Length 114;  
Best Local Similarity 98.4%; Pred. No. 1.6e-31;  
Matches 62; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 KIREYKSKRQTSQGVADASSYQOELERELFKLKQMGADNMTFFTFKFEDEPKFEVLEK 73  
Db 52 KIREYKSKRQTSQGVADASSYQOELERELFKLKQMGADNMTFFTFKFEDEPKFEVLEK 111  
QY 74 POA 76  
Db 112 POA 114

RESULT 10  
US-08-828-239-5  
; Sequence 5, Application US/08828239  
; Patent No. 5849527  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: NOVEL ATP SYNTHASE COUPLING FACTOR 6  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/828,239  
FILING DATE: Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0260 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 203530  
US-08-828-239-5

Query Match 80.5%; Score 317; DB 2; Length 108;  
Best Local Similarity 75.0%; Pred. No. 1.4e-30;  
Matches 57; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 NKEIDPIOKLFVDKIREYKSRQTSGGPVDASSFYQOELERELFKLKMFGNADMTPT 60  
DB 33 NKEIDPVQKLFIDKIREYKARLASGGPVDGPEYQOEVDRLEFLKMYGKGEMDKPT 92  
QY 61 FKPEDPKFEVLKPKQA 76  
DB 93 FNFEDPKFEVLDPKPS 108

RESULT 11  
US-09-205-679-5  
Sequence 5, Application US/09205679  
Patent No. 6048718  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Shah, Purvi  
TITLE OF INVENTION: NOVEL ATP SYNTHASE COUPLING FACTOR 6  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/205,679  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/828,239  
FILING DATE: 03/31/1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0260 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 108 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 203530  
US-09-205-679-5

Query Match 80.5%; Score 317; DB 3; Length 108;  
Best Local Similarity 75.0%; Pred. No. 1.4e-30;  
Matches 57; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 NKEIDPIOKLFVDKIREYKSRQTSGGPVDASSFYQOELERELFKLKMFGNADMTPT 60  
DB 33 NKEIDPVQKLFIDKIREYKARLASGGPVDGPEYQOEVDRLEFLKMYGKGEMDKPT 92  
QY 61 FKPEDPKFEVLKPKQA 76  
DB 93 FNFEDPKFEVLDPKPS 108

RESULT 12  
US-09-513-999C-5968  
Sequence 5968, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Mline Edwards, J.B.  
APPLICANT: Duclet, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
Patent No. 6783961  
FILE REFERENCE: 59. US2. REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 5968  
LENGTH: 69  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: 65  
OTHER INFORMATION: Xaa-Pro or Ser  
US-09-513-999C-5968

Query Match 47.0%; Score 185; DB 4; Length 69;  
Best Local Similarity 97.3%; Pred. No. 5.3e-15;  
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NKEIDPIOKLFVDKIREYKSRQTSGGPVDASSFYQO 37  
DB 33 NKEIDPIOKLFVDKIREYKSRQTSGGPVDASSFYQO 69

RESULT 13  
US-09-538-092-901  
Sequence 901, Application US/09538092  
Patent No. 675314  
GENERAL INFORMATION:  
APPLICANT: Gluc, Loic  
APPLICANT: Mansfield, Traci A.  
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

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FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: Curataseqformater Version 0.9
SEQ ID NO 901
LENGTH: 1940
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P11055
US-09-538-092-901
```

```
Query Match 20.2%; Score 79.5; DB 4; Length 1940;
Best Local Similarity 33.3%; Pred. No. 1.4;
Matches 22; Conservative 13; Mismatches 30; Indels 1; Gaps 1;
```

```
QY 4 LDP1QKLFVDKIRKRYKSKRQTSGGPVDASSEYQOELERELFKLKMGFNGADMTPTPFKF 63
DB 1443 LDKKQRFNDKVLAEWKTKCESQALEKSLKESRSLSTELFKLKNAYEEA-LDQLETVKR 1501
QY 64 EDPKFE 69
DB 1502 ENKNLE 1507
```

```
RESULT 14
US-09-949-016-8888
Sequence 8888, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8888
LENGTH: 1963
TYPE: PRT
ORGANISM: Human
US-09-949-016-8888
```

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Query Match 20.2%; Score 79.5; DB 4; Length 1963;
Best Local Similarity 33.3%; Pred. No. 1.4;
Matches 22; Conservative 13; Mismatches 30; Indels 1; Gaps 1;
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QY 4 LDP1QKLFVDKIRKRYKSKRQTSGGPVDASSEYQOELERELFKLKMGFNGADMTPTPFKF 63
DB 1466 LDKKQRFNDKVLAEWKTKCESQALEKSLKESRSLSTELFKLKNAYEEA-LDQLETVKR 1524
QY 64 EDPKFE 69
DB 1525 ENKNLE 1530
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```
RESULT 15
US-08-938-105-3
Sequence 3, Application US/08938105
```

```
Patent No. 6353151
GENERAL INFORMATION:
APPLICANT: Leinwand, Leslie A.
APPLICANT: Vikstrom, Karen L.
TITLE OF INVENTION: TRANSGENIC MODEL FOR HEART FAILURE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: CO
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,105
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Crook, Wanneil M.
REGISTRATION NUMBER: 31,071
REFERENCE/DOCKET NUMBER: 3595-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1886 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-938-105-3
```

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Query Match 19.2%; Score 75.5; DB 3; Length 1886;
Best Local Similarity 30.3%; Pred. No. 4.1;
Matches 20; Conservative 13; Mismatches 32; Indels 1; Gaps 1;
```

```
QY 4 LDP1QKLFVDKIRKRYKSKRQTSGGPVDASSEYQOELERELFKLKMGFNGADMTPTPFKF 63
DB 1391 LDKKQRFNDKVLAEWKTKCESQALEKSLKESRSLSTELFKLKNAY-EESSHLETVKR 1449
QY 64 EDPKFE 69
DB 1450 ENKNLQ 1455
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Search completed: April 4, 2005, 18:59:20
Job time : 31 secs
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